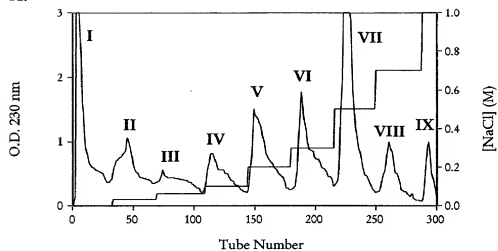
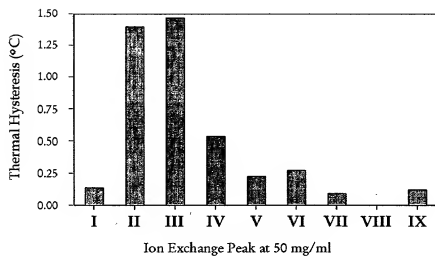


Fig. 1.0

A.**B.***Fig. 1.1*

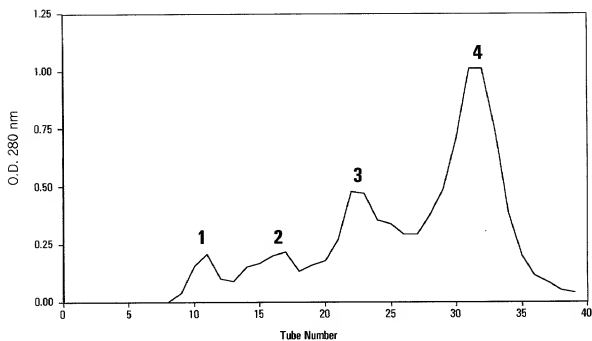


Fig. 1.2

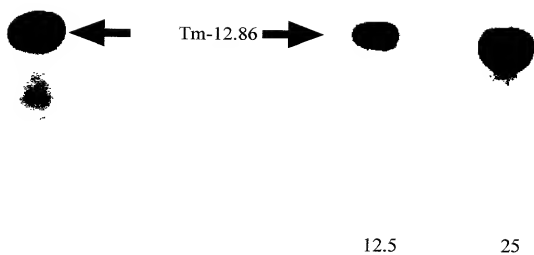


Fig. 1.3

Fig. 1.4

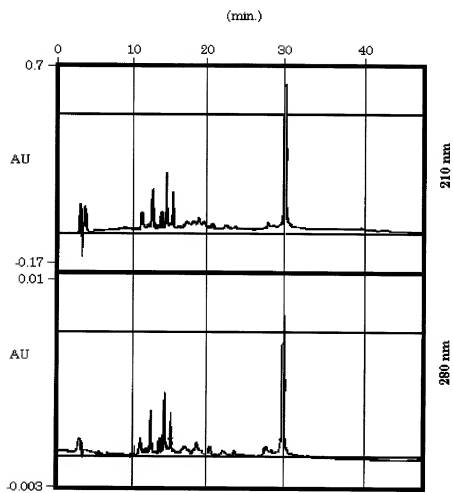


Fig. 1.5

09075705-01200

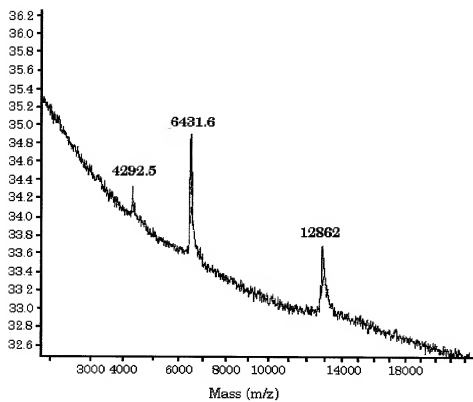


Fig. 1.6

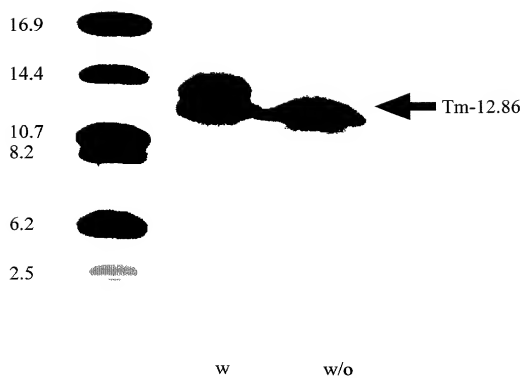
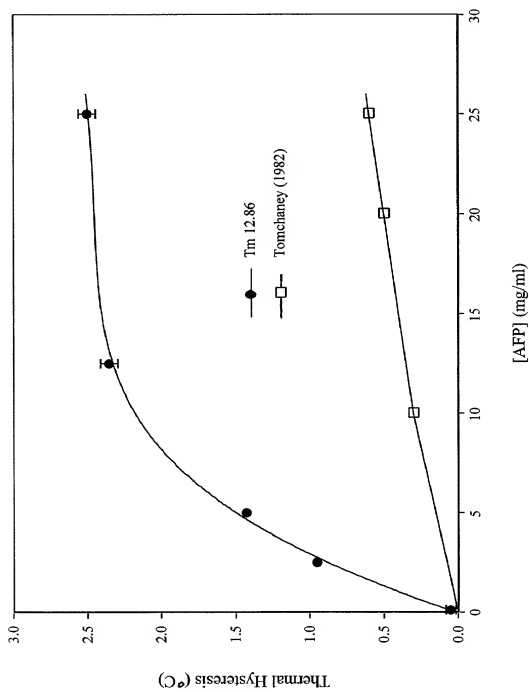


Fig. 1.7

NH_2 -L-T-D-E-Q-I-Q-K-R-N-K-I-S-K-E-?-Q-Q-V
 Val
 Gln
 Gln
 Glu
 Lys
 Ser
 Ile
 Lys
 Asn
 Arg
 Lys
 Gln
 Gln
 Ile
 Glu
 Glu
 Asp
 Thr
 Leu

Fig. 1.8

*Fig. 1.9*

09876796.021302

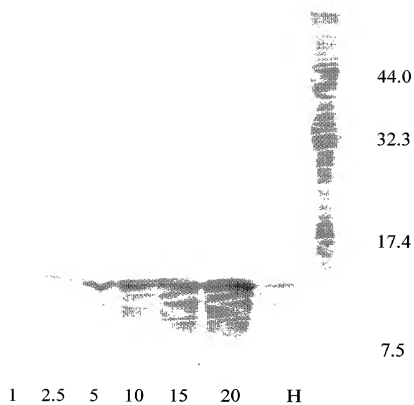
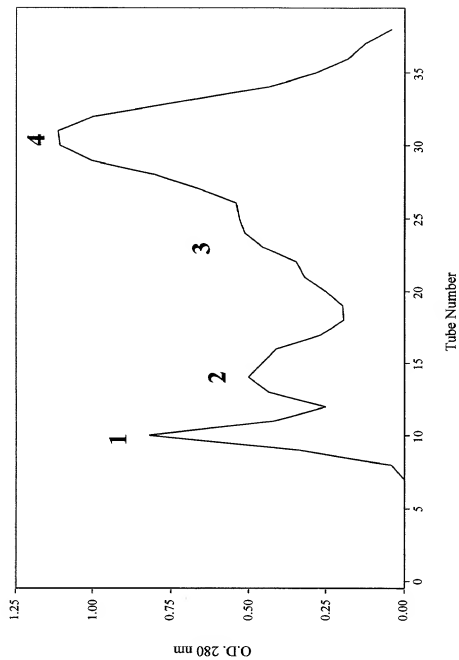
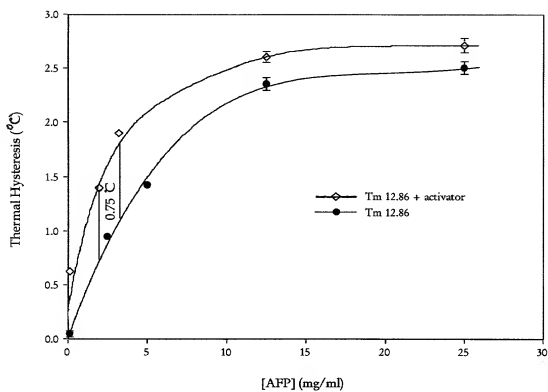
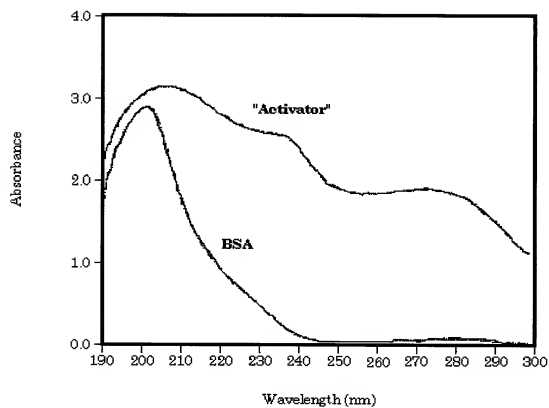


Fig. 1.10

*Fig. 1.11*

*Fig. 1.12*

*Fig. 1.13*

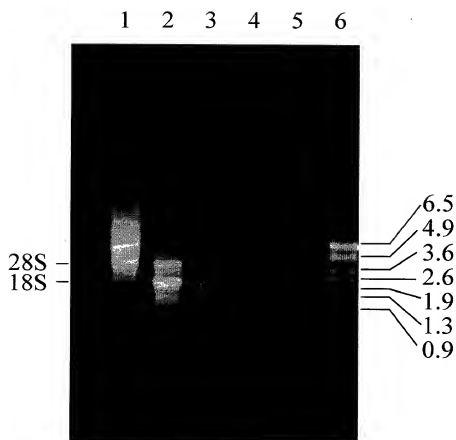
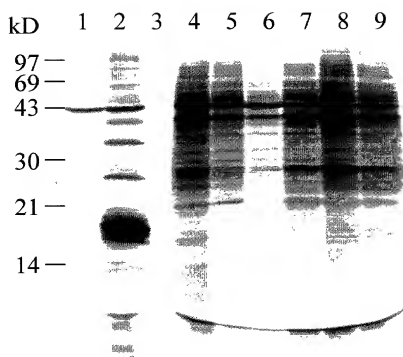
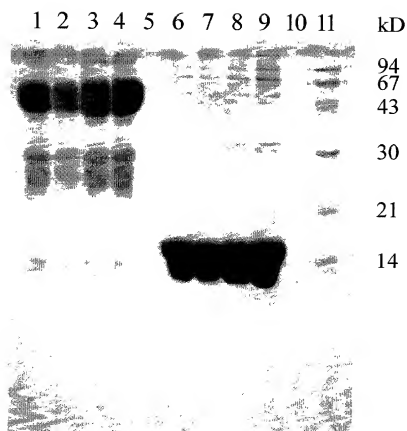


Fig. 2.0

*Fig. 2.1*

*Fig. 2.2*

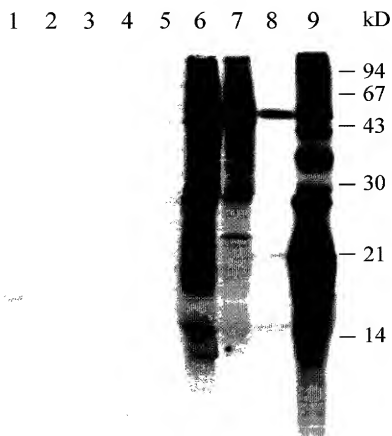


Fig. 2.3

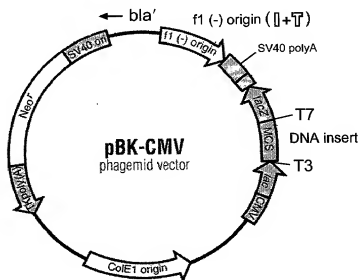
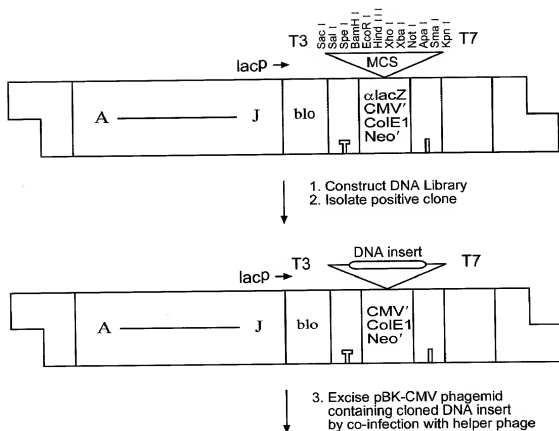


Fig. 2.4a

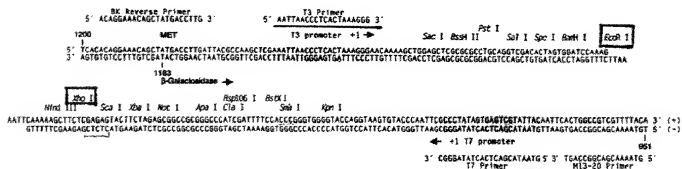
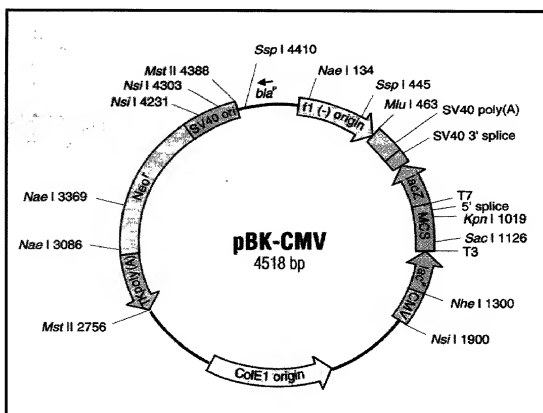


Fig 2.46

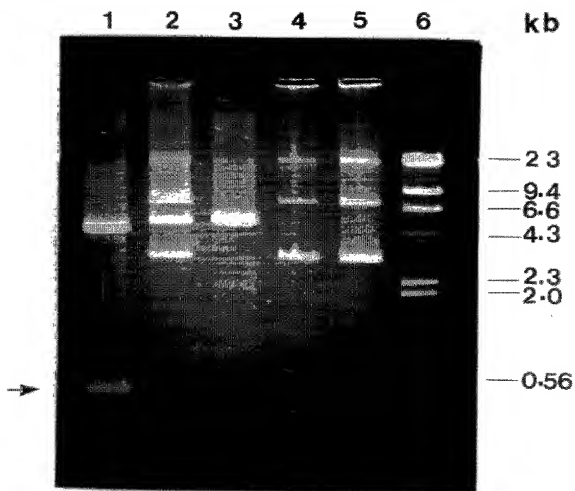


Fig. 2.5

DNA sequence of Tm 13.17 cDNA clone

B E
 a c
 m o
 H R
 I I

1 AGTGGATCCAAAGAATTTCGGCAGGAGACTACTAAGCTGAGTTGCTCTGTTGTCTAATCT
 M K L L C C L I S

61 CCCTCATTCTGTTGGTCACAGTTCAGGCCCTGACCGAGGCACAAATTGAGAACTGAACA
 L I L L V T V Q A L T E A Q I E K L N K

121 AGATCAGCAAAAAATGTCAAAATGAAAGTGGAGTGTGCGCAAGAGATCATAACCAAAGCTC
 I S K K C Q N E S G V S Q E I I T K A R

181 GCAACGGTGACTGGGAGGACGATCCTAAACTGAAACGCCAAGTTTTTTGCGGTGGCCAGGA
 N G D W E D D P K L K R Q V F C V A R N

241 ACGCCGGTCTGGCCACGGAATCGGGAGAGGTGGTGGTGCACGTGTTGAGGGAGAGGTGA
 A G L A T E S G E V V V D V L R E K V R

301 GGAAGGTCACTGACAACGACGAAGAACTGAGAAATCATCAATAAGTGCGCCGTCAAGA
 K V T D N D E E T E K I I N K C A V K R

361 GAGATACTGTTGAAGAGACGGTGTTCATACTTTCAAATGTGTGATGAAAAACAAGCCAA
 D T V E E T V F N T F K C V M K N K P K

421 AGTTCTCACCAAGTTGATTGAACCAACCGACTAGTAGATGGTTCAAATGGTGTGCTTTAC
 F S P V D *

481 ATATAAAAAATAAAGTGTTCGTGATGTAAAAAATAAAAAAAAAAAAAAAAAAACTCG
 polyadenylation signal poly (A) tail (26)

537 AGAGTATTCTAGAGCGGCCCGGGGCCATCGTTTCCACCC

x
 h
 o
 i

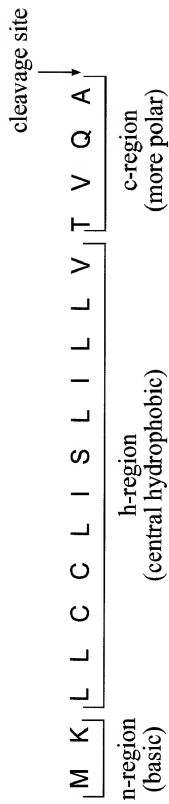


Fig. 2.66

[illegible]

B. Summary of the composition analysis for the mature Tm 13.17 sequence:

<u>Residue</u>	<u>Number</u>	<u>Mole Percent</u>
A = Ala	6	5.172
B = Asx	0	0.000
C = Cys	4	3.448
D = Asp	8	6.897
E = Glu	13	11.207
F = Phe	4	3.448
G = Gly	4	3.448
H = His	0	0.000
I = Ile	6	5.172
K = Lys	16	13.793
L = Leu	5	4.310
M = Met	1	0.862
N = Asn	8	6.897
P = Pro	3	2.586
Q = Gln	4	3.448
R = Arg	6	5.172
S = Ser	5	4.310
T = Thr	8	6.897
V = Val	14	12.069
W = Trp	1	0.862
Y = Tyr	0	0.000
Z = Glx	0	0.000

Molecular weight = 13171.96; Residues = 116; Average Residue Weight = 113.551

Charge = 1; Isoelectric point = 7.74.

Fig. 2.6c

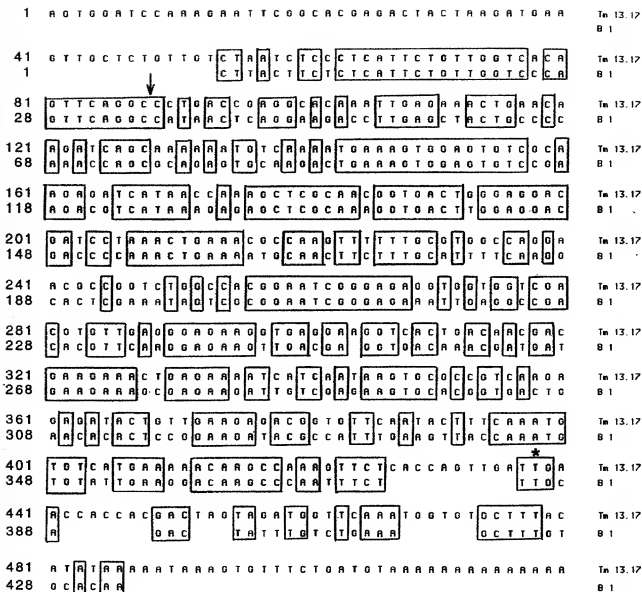


Fig. 2.7

Tm 13.17	3	EAQIEKLNKISKKQNESGVSEIITKARNGDWEDDPKLRQVFCVARNA	52
	 :: :.. : :. : :	
AFP-3	1	ETPREKLQHSACKAESGVSESLNKVRNREEVDDPKLKEHAFCLKRA	50
Tm 13.17	53	GLATESGEVVVDVLRKVRKVTNDDEETEKIINKCAVKRDTVEETVFNTF	102
		: .. . : :: .:. :.. :: ... :	
AFP-3	51	GFIDASGEFQLDHIKTKFKENSEHPEKVDLDLAKCAVKKDTQPQHSSADPF	100
Tm 13.17	103	KCVMKNKP	110
		. :.	
AFP-3	101	KCVHDNRS	108

Percent identity: 39.8 (identical amino acids; Percent similarity: 58.3 (identical amino acids plus conservative amino acids).

Fig. 2.8

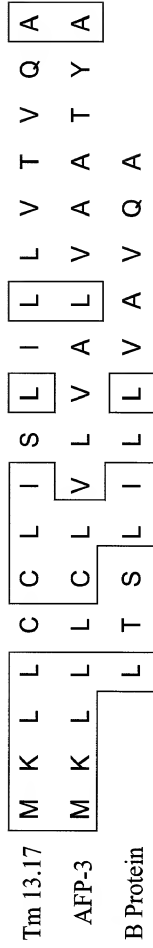


Fig. 2.9

Tm 13.17	NH2	L	T	E	A	Q	I	E	K	L	N	K	I	S	K	K	C	Q	N	E
		:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:
Tm 12.86	NH2	L	T	D	E	Q	I	Q	K	R	N	K	I	S	K	E	?	Q	Q	V

Fig 2.10

09876796.021202

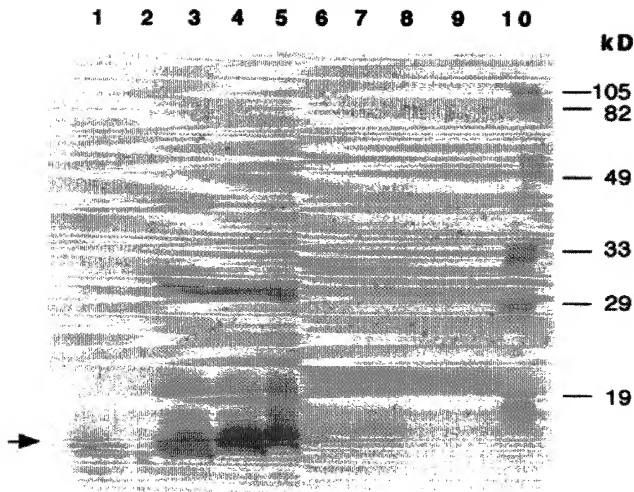


Fig 2.11

Tm 12.86 L T D E Q I Q K R N K I S K E ? Q Q V
 Tm 13.17 1 L T E A Q I E K L N K I S K K C Q N E S G V S Q E I I T K A
 B1 13 I T E E D L E L L R Q T S A E C K T E S G V S E D V I K R A
 AFP-3 1 E T P R E K L K Q H S D A C K A E S G V S E E S L N K V

Tm13.17 31 R N G D W E D D P K L K R Q V F C V A R N A G L A T E S G E
 B1 44 R K G D L E D D P K L K M Q L L C I F K A L E I V A E S G E
 AFP-3 29 R N R E E V D D P K L K E H A F C I L K R A G F I D A S G E

Tm13.17 61 V V V D V L R E K V R K V T D N D E E T E K I I N K C A V K
 B1 75 I E A D T F K E K L T R V T N D D E E S E K I V E K C T V T
 AFP-3 59 F Q L D H I K T K F K E N S E H P E K V D D L V A K C A V K

Tm13.17 91 R D T V E E T V F N T F K C V M K N K P K F S P V D
 B1 106 E D T P E D T A F E V T K C V L K D K P N F F G D L F V
 AFP-3 89 K D T P Q H S S A D F F K C V E D N R S

Fig. 2.12

polyadenylation signal

Fig. 3.0

polyadenylation signal

Fig 3.1

Start

↓

2-2 GGCACGAGCAAAAATGAAACTCCTCTTGTGCTTTGC[G]
 2-3 GGCACGAGCAAAAATGAAACTCCTCTTGTGCTTTGC[T]

2-2 TTCGCCGCCATCGTCATCGGAGCTCAGGCTCTCACCG
 2-3 TTCGCCGCCATCGTCATCGGAGCTCAGGCTCTCACCG

2-2 ACGAACAGATACAGAAAAGGAACAAGATCAGCAAAGA
 2-3 ACGAACAGATACAGAAAAGGAACAAGATCAGCAAAGA

2-2 ATGCCAGCAGGTGTCCGGAGTGTCCCAAGAGACGATC
 2-3 ATGCCAGCAGGTGTCCGGAGTGTCCCAAGAGACGATC

2-2 GACAAAGTCCGCACAGGTGTCTTGGTCGA[T]GATCCCA
 2-3 GACAAAGTCCGCACAGGTGTCTTGGTCGA[C]GATCCCA

2-2 AAATGAAGAAAGCACGTCCTCTGCTTCTCGAAGAAAAC
 2-3 AAATGAAGAAAGCACGTCCTCTGCTTCTCGAAGAAAAC

2-2 TGGAGTGGCAACCGAAGCCGGAGACACCAATGTGGAG
 2-3 TGGAGTGGCAACCGAAGCCGGAGACACCAATGTGGAG

2-2 GTACTCAAAGCCAAGCTGAAGCATGTGGCCAGCGACG
 2-3 GTACTCAAAGCCAAGCTGAAGCATGTGGCCAGCGACG

2-2 AAGA[G]GTGGACAAGATCGTGCAGAAAGTGC GTGGTCAA
 2-3 AAGA[A]GTGGACAAGATCGTGCAGAAAGTGC GTGGTCAA

2-2 GAAGGCCACACCCAGAGGAAACGGCTTATGACACCTTC
 2-3 GAAGGCCACACCCAGAGGAAACGGCTTATGACACCTTC

2-2 AAGTGTATTTACGACAG[C]AAACCTGATTTCTCTCCTA
 2-3 AAGTGTATTTACGACAG[T]AAACCTGATTTCTCTCCTA

2-2 TTGATTAAATTTGTTTTGTATTTGACTGAATTTTGACAA
 2-3 TTGATTAAATTTGTTTTGTATTTGACTGAATTTTGACAA

2-2 TAAAGGTA[A]TATCGTTATG[T]AAAAA
 2-3 TAAAGGTA[C]TATCGTTATG[A]AAAAA

Fig 3.2

Predicted Amino Acid

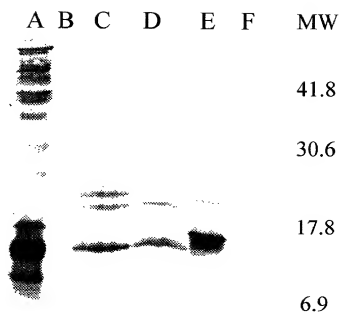
Composition of 2-2 and 2-3

Analysis	Whole Protein
Molecular Weight	12643.80 m.w.
Length	115
1 microgram =	77.859 pMoles
Molar Extinction coefficient	3040±5%
1 A(280) =	4.22 mg/ml
Isoelectric Point	7.11
Charge at pH 7	0.13

Whole Protein Composition Analysis

Amino Acid(s)	Number count	% by weight	% by frequency
Charged (RKHYCDE)	48	47.19	41.74
Acidic (DE)	20	18.90	17.39
Basic (KR)	20	20.40	17.39
Polar (NCQSTY)	30	25.35	26.09
Hydrophobic (AILFWV)	34	27.26	29.57
A Ala	6	3.32	5.22
C Cys	4	3.21	3.48
D Asp	11	9.86	9.57
E Glu	9	9.05	7.83
F Phe	3	3.44	2.61
G Gly	4	1.78	3.48
H His	2	2.14	1.74
I Ile	6	5.29	5.22
K Lys	18	17.97	15.65
L Leu	5	4.41	4.35
M Met	1	1.02	0.87
N Asn	2	1.78	1.74
P Pro	4	3.02	3.48
Q Gln	6	5.98	5.22
R Arg	2	2.43	1.74
S Ser	7	4.75	6.09
T Thr	9	7.08	7.83
V Val	14	10.80	12.17
W Trp	0	0.00	0.00
Y Tyr	2	2.54	1.74
B Asx	0	0.00	0.00
Z Glx	0	0.00	0.00
X Xxx	0	0.00	0.00
. Ter	0	0.00	0.00

Fig. 3.3

*Fig. 3.4*

Lane

1 2 3 4 5



Fig. 4.0

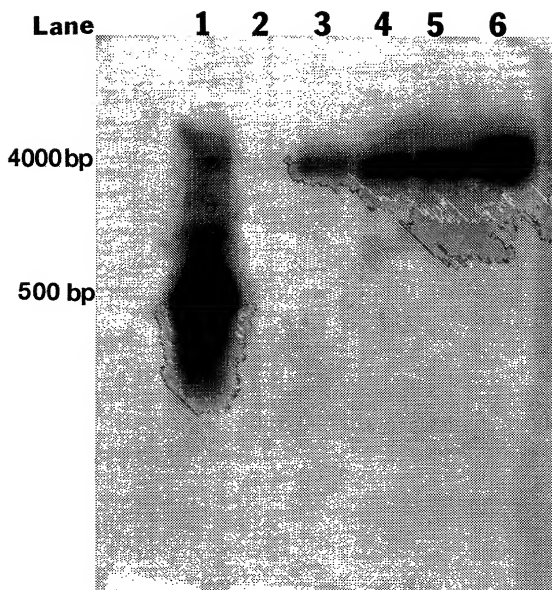
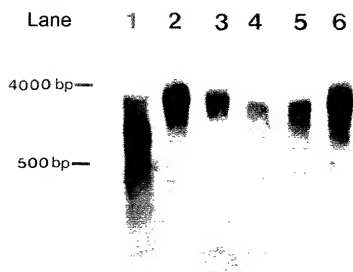
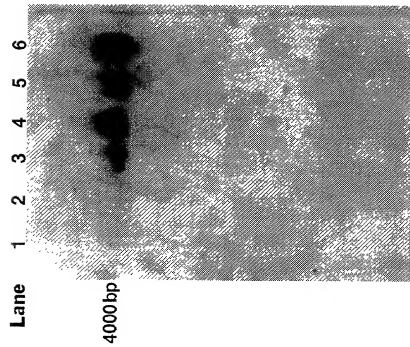
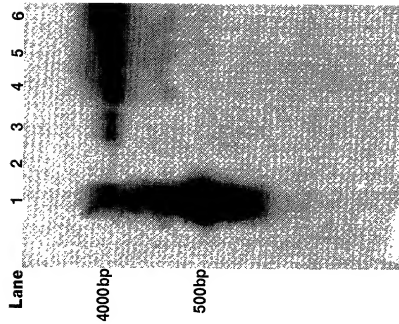


Fig. 4.1

*Fig. 4.2*

A.**B.***Fig. 4.3*

202120.96/9/86

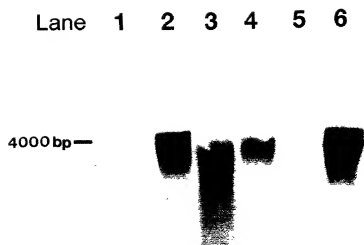


Fig. 4.4

Lane

1

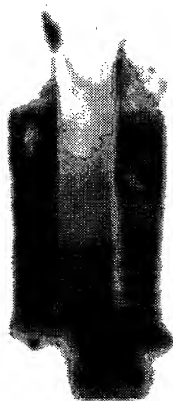
2

3

4

5

09876796-021202



23130

9416

4361

2322

2027

564

Fig. 4.5

Tm 13.17 cDNA

1 AGTGGATCCAAAGAATTTCGGCAGGAGACTACTAAGATGAGTTGCTCTGTTGTCTAATCT
M K L L C C L I S

61 CCTCATTTCTGTTGGTCACAGTTCAGGCCCTGACCGAGGCACAAATTGAGAACTGAACA
L I L L V T V Q A L T E A Q I E K L N K
↑ Forward Primer

121 AGATCAGCAAAAAATGTCAAAATGAAAGTGGAGTGTTCGCAAGGATCATAACCAAAGCTC
I S K K C Q N E S G V S Q E I I T K A R

181 GCAACGGTGACTGGGAGGACGATCCTAAACTGAAACGCCAAGTTTTCGCGTGCCAGGA
N G D W E D D P K L K R Q V F C V A R N

241 ACGCCGGTCTGGCCACGGAATCGGGAGAGGTGGTGGTCGACGTGTTGAGGGAGAAGGTGA
A G L A T E S G E V V V D V L R E K V R

301 GGAAGGTCACTGACAAACGACGAAGAACTGAGAAAATCATCAATAAGTGCGCCCTCAAGA
K V T D N D E E T E K I I N K C A V K R
Reverse Primer

361 GAGATACTGTTGAAGAGACGGGTGTTCAATACTTTCAAATGTGTCATGAAAAACAAGCCAA
D T V E E T V F N T F K C V M K N K P K

421 AGTTCTCACCAGTTGATTGAACCACCAGACTAGTAGATGGTTCAAATGGTGTGCTTTAC
F S P V D *

481 ATATAAAAAATAAAGTGTCTTCTGATGTAAAAAATAAAAAAAAAAAAAAAAAAACTCG
polyadenylation signal poly (A) tail (26)

537 AGAGTATTCTAGAGCGGCCGCGGGCCCATCGTTTTCCACCC

Fig. 4.6a

Forward Primer

2-2 L T D E O I Q K R N K I S K E C Q Q V S G V S Q E T I D K V R T G V L V
 Tm 13.17 L T E A O I E K L N K I S K K C Q N E S G V S Q E I I T K A R N G D W E
 B2 L T E E D L O L L R O T S A E C K T E S G A S E A V I K K A R K G D L E
 AFP-3 E T P R E K L K Q H S D A C K A E S G V S E E S L N K V R N R E E V

2-2 D D P K M K K H V L C F S K K T G V A T E A G D T N V E V L K A K L K H
 Tm 13.17 D D P K L K R Q V F C V A R N A G L A T E S G E V V V D V L R E K V R K
 B2 D D P K L K M Q L L C I F K A L E I V A E S G E I E A D T F K E K L T R
 AFP-3 D D P K L K E H A F C I L K R A G F I D A S G E F Q L D H I K T K F K E

Reverse Primer

2-2 V A S D E E V D K I V Q K C V V K K A T P E E T A Y D T F K C I Y D S
 Tm 13.17 V T D N D E E T E K I I N K C A V K R D T V E E T V F N T F K C V M K N
 B2 V T N D D E E S E K I V E K C T V T E D T P E D T A F E V T K C V L K D
 AFP-3 N S E H P E K V D D L V A K C A V K K D T P Q H S S A D F F K C V H D N

2-2 K P D F S P I D
 Tm 13.17 K P K F S P V D
 B2 K P N F F G D L F V
 AFP-3 R S

Fig. 4.6b

Primer	percent % composition				Melting Temperature (°C)
	A	C	G	T	
Forward	28.6	14.3	42.9	14.3	44.0
Reverse	25.0	31.3	6.3	37.5	44.0

Fig. 4.6c

09876796.021202

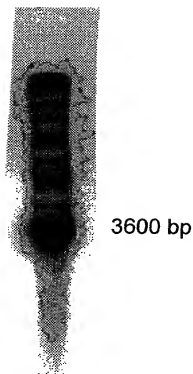


Fig. 4.7

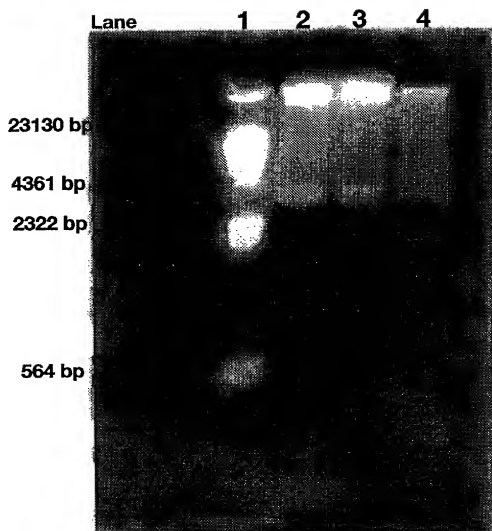


Fig. 4.8

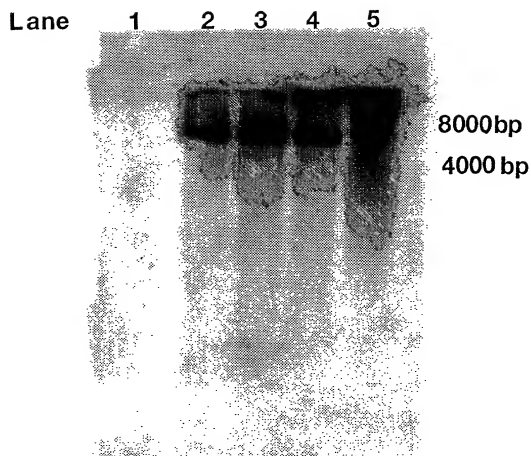


Fig. 4.9

1 GGCACGAGCAAAA ATGAAACTCCTCTTGTGCTTTGCTTTGCGCGCC
 M K L L L C F A F A A
 47 ATCGTCATCGGAGCTCAGGCTCTCACCGACGAACAGATACAGAAA
 I V I G A Q A L T D E Q I Q K
 92 AGGAACAAGATCAGCAAAGAATGCCAGCAGGTGTCCGGAGTGTCC
 R N K I S K E C Q Q V S G V S
 137 CAAGAGACGATCGACAAAGTCCGCACAGGTGTCTTGGTCGACGAT
 Q E T I D K V R T G V L V D D
 182 CCCAAAATGAAGAAGCACGTCCTCTGCTTCTCGAAGAAAACCTGGA
 P K M K K H V L C F S K K T G
 226 GTGGCAACCGAAGCCGGAGACACCAATGTGGAGGTACTCAAAGCC
 V A T E A G D T N V E V L K A
 271 AAGCTGAAGCATGTGGCCAGCAGCAAGAGGTGGACAAGATCGTG
 K L K H V A S D E E V D K I V
 316 CAGAAGTGC GTGGTCAAGAAGGCCACACCAAGGAAACGGCTTAT
 Q K C V V K K A T P E E T A Y
 361 GACACCTTCAAGGTTATTTACGACAGTAAACCTGATTTCTCTCCT
 D T F K V I Y D S K P D F S P
 406 ATTGATTAA TTGTTTTGTATTTGACTGAATTTTGACAATAAAGGT
 I D
 451 ACTATCGTTATGTA AAAAAAAAAAAAAAAAAA polyadenylation signal

poly (A) tail

Fig. 4.10a

1 GGCACGAGCAAAAATGAAACTCCTCTTGTGCTTTGCTTTCGCCGCC
 M K L L L C F A F A A
 47 ATCGTCATCGGAGCTCAGGCTCTCACCGATGAACAGATACAGAAA
 I V I G A Q A L T D E Q I Q K
 92 AGGAACAAGATCAGCAAAGAATGCCAGCAGGAGTCCGGAGTGTCC
 R N K I S K E C Q Q E S G V S
 137 CAAGAGACGATCGACAAAGTCCGCACAGGTGTCTTGGTCGACGAT
 Q E T I D K V R T G V L V D D
 182 CCCAAAATGAAGAAGCACGTCCTCTGCTTCTCGAAGAGAAGTGGGA
 P K M K K H V L C F S K R T G
 226 GTGGCAACCGAAGCCGGAGACACCAATGTGGAGGTACTCAAAGCC
 V A T E A G D T N V E V L K A
 271 AAGCTGAAGCATGTGGCCAGCGACGAAGAAGTGGACAAGATCGTG
 K L K H V A S D E E V D K I V
 316 CAGAAGTGCCTGGTCAAGAAGGCCACACCAGAGGAAACGGCTTAT
 Q K C V V K K A T P E E T A Y
 361 GACACCTTCAAGTGTATTTACGACAGTAAACCTGATTTCTCTCCT
 D T F K V I Y D S K P D F S P
 406 ATTGATTAAATTGTTTTGTATTTGACTGAATTTGACAATAAAGGT
 I D .
 451 ACTATCGTTATGAAAAAAAAAAAAAAAAAAAAA

polyadenylation signal

poly (A) tail

Fig. 4.11a

Predicted Amino Acid

Composition of 3-9

Analysis	Whole Protein
Molecular Weight	12871.80 m.w.
Length	115
1 microgram =	77.689 pMoles
Molar Extinction coefficient	3040±5%
1 A(280) =	4.23 mg/ml
Isoelectric Point	7.11
Charge at pH 7	0.13

Whole Protein Composition Analysis

Amino Acid(s)	Number count	% by weight	% by frequency
Charged (RKHYCDE)	48	47.31	41.74
Acidic (DE)	20	18.86	17.39
Basic (KR)	20	20.57	17.39
Polar (NCQSTY)	30	25.29	26.09
Hydrophobic (AILFWV)	34	27.20	29.57
A Ala	6	3.31	5.22
C Cys	4	3.21	3.48
D Asp	11	9.84	9.57
E Glu	9	9.03	7.83
F Phe	3	3.43	2.61
G Gly	4	1.77	3.48
H His	2	2.13	1.74
I Ile	6	5.28	5.22
K Lys	17	16.93	14.78
L Leu	5	4.40	4.35
M Met	1	1.02	0.87
N Asn	2	1.77	1.74
P Pro	4	3.02	3.48
Q Gln	6	5.97	5.22
R Arg	3	3.64	2.61
S Ser	7	4.74	6.09
T Thr	9	7.07	7.83
V Val	14	10.78	12.17
W Trp	0	0.00	0.00
Y Tyr	2	2.54	1.74
B Asx	0	0.00	0.00
Z Glx	0	0.00	0.00
X Xxx	0	0.00	0.00
. Ter	0	0.00	0.00

Fig. 4.11b

polyadenylation signal

Fig. 4.12a

Predicted Amino Acid

Composition of 7-5

Analysis	Whole Protein
Molecular Weight	12843.80 m.w.
Length	115
1 microgram =	77.859 pMoles
Molar Extinction coefficient	3040±5%
1 A(280) =	4.22 mg/ml
Isoelectric Point	7.11
Charge at pH 7	0.13

Whole Protein Composition Analysis

Amino Acid(s)	Number count	% by weight	% by frequency
Charged (RKHYCDE)	48	47.19	41.74
Acidic (DE)	20	18.90	17.39
Basic (KR)	20	20.40	17.39
Polar (NCGSTY)	30	25.35	26.09
Hydrophobic (AILFWV)	34	27.26	29.57
A Ala	6	3.32	5.22
C Cys	4	3.21	3.48
D Asp	11	9.86	9.57
E Glu	9	9.05	7.83
F Phe	3	3.44	2.61
G Gly	4	1.78	3.48
H His	2	2.14	1.74
I Ile	6	5.29	5.22
K Lys	18	17.97	15.65
L Leu	5	4.41	4.35
M Met	1	1.02	0.87
N Asn	2	1.78	1.74
P Pro	4	3.02	3.48
Q Gln	6	5.98	5.22
R Arg	2	2.43	1.74
S Ser	7	4.75	6.09
T Thr	9	7.08	7.83
V Val	14	10.80	12.17
W Trp	0	0.00	0.00
Y Tyr	2	2.54	1.74
B Asx	0	0.00	0.00
Z Glx	0	0.00	0.00
X Xxx	0	0.00	0.00
. Ter	0	0.00	0.00

Fig. 4.12b

20250706 09:27:06



MKLLLCFAFAAIVIGACALTDEQIQKRNKISKECCQCVSGGVSGQETIDKVRTGVLV
 MKLLLCFAFAAIVIGACALTDEQIQKRNKISKECCQCVSGGVSGQETIDKVRTGVLV
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 MKLLLCFAFAAIVIGACALTDEQIQKRNKISKECCQCVSGGVSGQETIDKVRTGVLV

2-2
 2-3
 3-4
 3-9
 7-5

DPPKMKKHVLCFESKKTGVATEAGD TNVEVLKAKLKHVAS DEEVVDKIVQKCVVKKK
 DPPKMKKHVLCFESKKTGVATEAGD TNVEVLKAKLKHVAS DEEVVDKIVQKCVVKKK
 DPPKMKKHVLCFESKKTGVATEAGD TNVEVLKAKLKHVAS DEEVVDKIVQKCVVKKK
 DPPKMKKHVLCFESKKTGVATEAGD TNVEVLKAKLKHVAS DEEVVDKIVQKCVVKKK

2-2
 2-3
 3-4
 3-9
 7-5

ATPEETAYDTFKCIIYDSKPD FSPID*
 ATPEETAYDTFKCIIYDSKPD FSPID*
 ATPEETAYDTFKCIIYDSKPD FSPID*
 ATPEETAYDTFKCIIYDSKPD FSPID*

2-2
 2-3
 3-4
 3-9
 7-5

Fig. 4.14

	MW (kDa)	AA (#)	(% mole)																% most hydrophobic				
			Cys	Pro	Phe	Ile	Val	Met	Leu	Gly Ala Tyr His					Trp	Asx	Glx	Arg		Lys	Ser	Thr	% most hydrophilic
Tm 12.86	12.86	117	3.2	3.0	3.4	4.4	8.5	2.0	4.4	28.9	3.1	3.9	3.8	3.2	ND	10.7	15.0	3.6	14.9	6.8	6.3	57.3	
Tm 13.17	13.17	116	3.13	2.21	4.47	5.16	10.5	1.0	4.3	29.11	1.73	3.24	0	0	1.41	0	0	7.12	15.6	3.31	6.14	32.14	
2-2	12.84	115	3.21	3.02	3.44	5.29	10.8	1.02	4.41	27.26	1.78	3.32	2.54	2.14	0	0	0	2.43	18.0	4.75	7.08	32.23	
2-3	12.84	115	3.21	3.02	3.44	5.29	10.8	1.02	4.41	27.26	1.78	3.32	2.54	2.14	0	0	0	2.43	18.0	4.75	7.08	32.23	
3-4	12.84	115	2.41	3.02	3.44	5.29	11.6	1.02	4.41	28.04	1.78	3.32	2.54	2.14	0	0	0	2.43	18.0	4.75	7.09	32.24	
3-9	12.87	115	3.21	3.02	3.43	5.28	10.8	1.02	4.40	27.20	1.77	3.31	2.54	2.13	0	0	0	3.64	16.9	4.74	7.07	32.38	
7-5	12.84	115	3.21	3.02	3.44	5.29	10.8	1.02	4.41	27.26	1.78	3.32	2.54	2.14	0	0	0	2.43	18.0	4.75	7.08	32.23	

Fig. 4.15

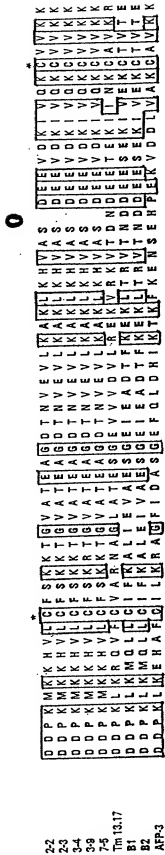
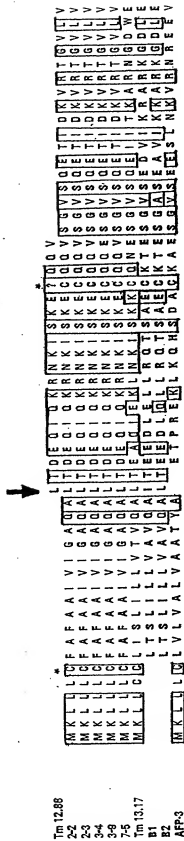


FIG 4.16
* = conserved cysteine (yellow)

conserved residues in ≥ 7 Genes (blue or orange)

Boxed

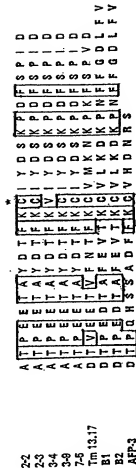
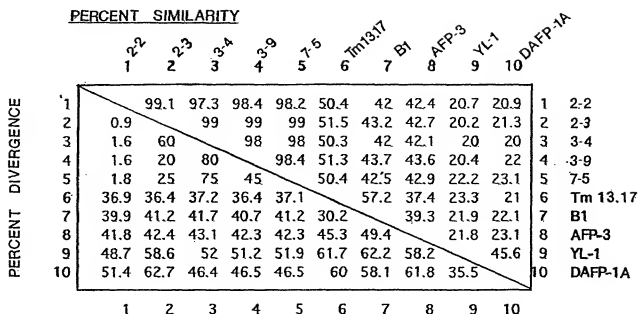


Fig. 4.16



Fig. 4.17

NUCLEOTIDE SEQUENCES



AMINO ACID SEQUENCES

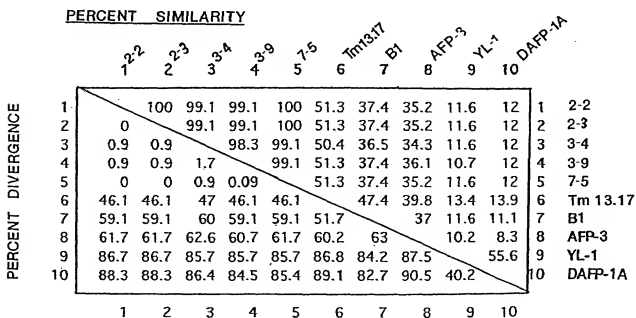
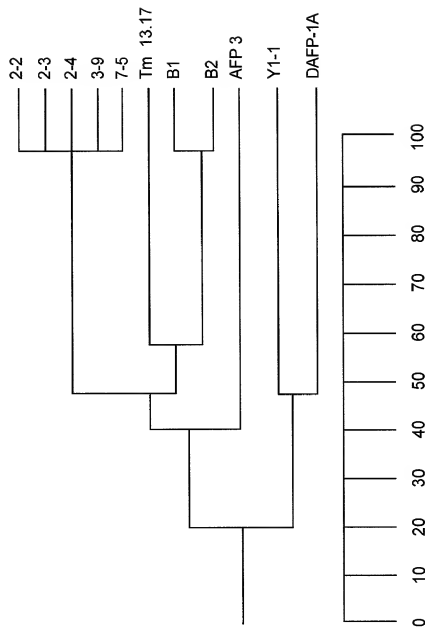


Fig. 4.19



% Nucleic Acid Identity

Fig. 4.20

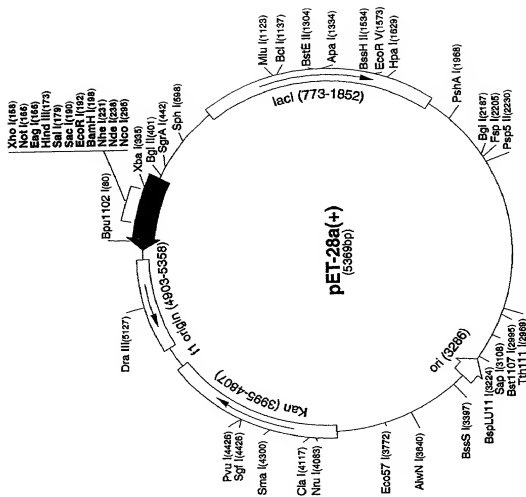


Fig. 5.0

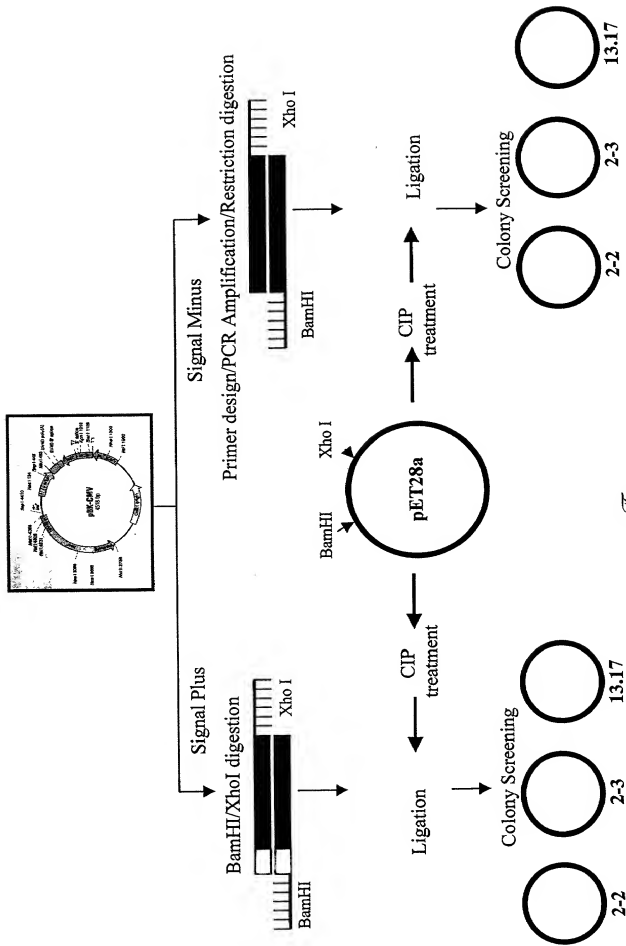


Fig. 5.1

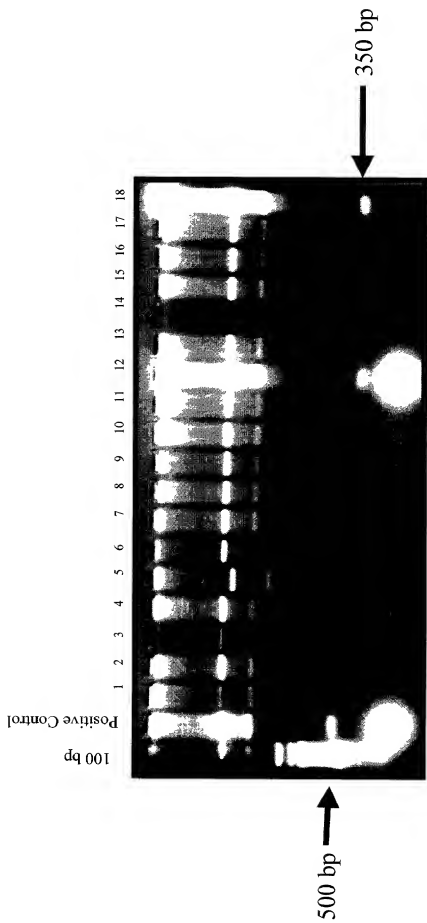


Fig. 5.2

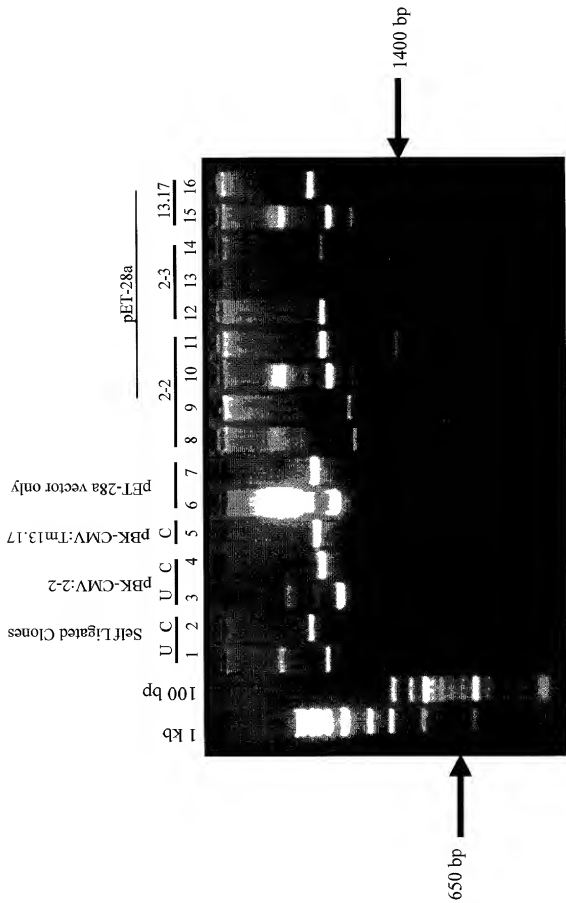


Fig. 5.3

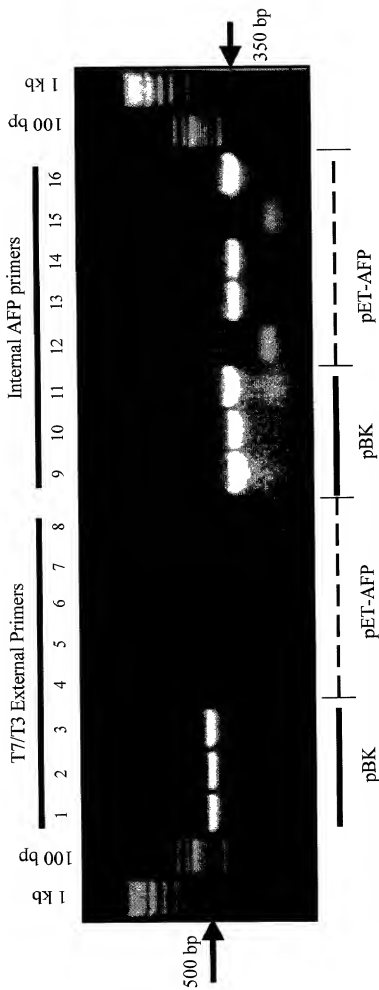


Fig. 5.4

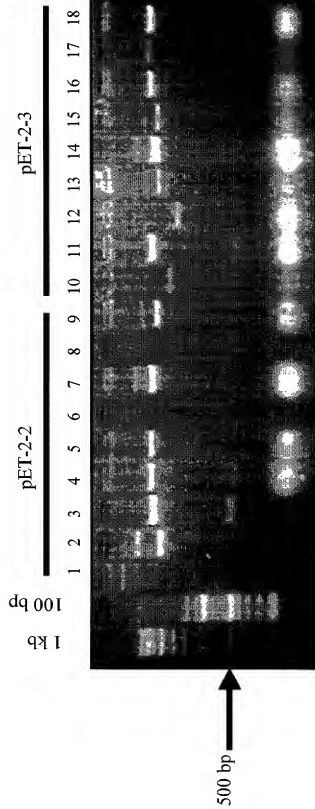


Fig. 5.5

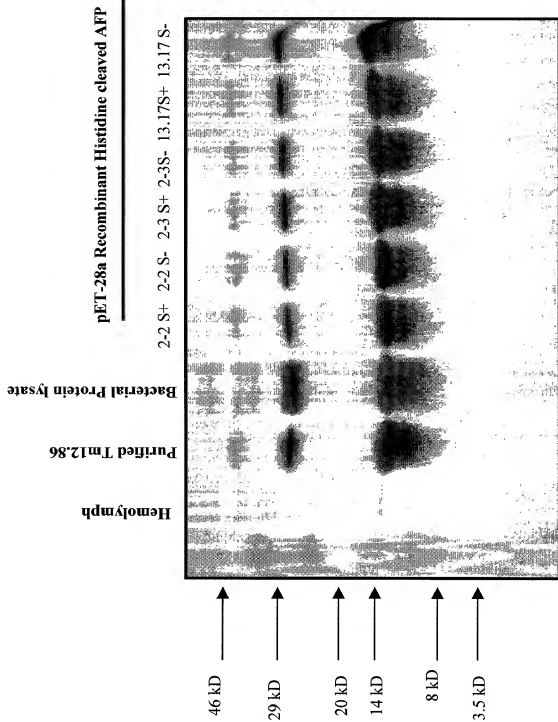


Fig. 5.6

His-tagged Clone 2.2 with signal sequence		
TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG	50	
His-tag Start Codon		
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC	96	
Met Gly Ser Ser His His His His His Ser	-55	-50
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT	141	
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly	-45	-40 -35
AFP Start Codon		
GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC GCA CGA GCA AAA ATG	186	
Gly Gln Gln Met Gly Arg Gly Ser Glu Phe Ala Arg Ala Lys Met	-30	-25 -20
AAA CTC CTC TTG TGC TTT GCG TTC GCC GCC ATC GTC ATC GGA GCT	231	
Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala	-15	-10 -5
N-terminal of mature AFP		
CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA AGC AAG ATC AGC	276	
Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser	1	5 10
AAA GAA TGC CAG CAG GTG TCC GGA GTG TCC CAA GAG ACG ATC GAC	321	
Lys Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp	15	20 25
AAA GTC CGC ACA GGT GTC TTG GTC GAT GAT CCC AAA ATG AAG AAG	366	
Lys Val Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys	30	35 40
CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA GTG GCA ACC GAA GCC	411	
His Val Leu Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala	45	50 55
GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC AAG CTG AAG CAT GTG	456	
Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu Lys His Val	60	65 70
GCC AGC GAC GAA GAG GTG GAC AAG ATC GTG CAG AAG TGC GTG GTC	501	
Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys Val Val	75	80 85
AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT GAC ACC TTC AAG TGT	546	
Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Lys Lys Cys	90	95 100
Stop Codon		
ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT ATT GAT TAA TTGTTTGTGA	595	
Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp *	105	110 115
Polyadenylation signal Poly-A tail		
TTTGACTGAA TTTTGACAAAT AAGGGTAATA TCGTTATGTA AAAAAAAAAA	645	
AAAAAAGCTG AGCAACCA CAACCAACAC TGAGAT	681	

Fig. 5.7

THE UNIVERSITY OF CHICAGO

50

ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC
Met Gly Ser Ser His His His His His His Ser

96

AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT 141
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly
-20 -15 -10

CTC ACC GAC GAA CAG ATA CAG
Leu Thr Asp Glu Gln Ile Gln
1 5

186

AAA AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GTG TCC GGA GTG 231
Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val
10 15 20

TCC CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAT 276
Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp
25 30 35

GAT CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT 321
Asp Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr
40 45 50

GGA GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA 366
Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys
55 60 65

GCC AAG CTG AAG CAT GTG GCC AGC GAC GAA GAG GTG GAC AAG ATC 411
Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile
70 75 80

GTG CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT 456
Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala
85 90 95

TAT GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT 501
Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser
100 105 110

CCT ATT GAT TAA CTCGAGCACC ACCACCACCA CCACTGAGAT
Pro Ile Asp *
115

543

His-tagged clone 2.3 with signal sequence		
TTGTTAGCGG ATGGAATCC CTCGTAGGGG ATAAATTTGT TTACTTTAAG	50	
His-tag Start Codon		
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAC AGC	96	
Met Gly Ser Ser His His His His His Ser		
-55 -50		
AGC GGC CTG GTG CGC CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT	141	
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly		
-45 -40 -35		
AFP Start Codon		
GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC GCA GCA AAA ATG	186	
Gly Gln Gln Met Gly Arg Gly Ser Glu Phe Ala Arg Ala Lys Met		
-30 -25 -20		
AAA CTC CTC TTG TGC TTT GCT TTC GCC GCC ATC GTC ATC GGA GCT	231	
Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala		
-15 -10 -5		
N-terminal of Mature AFP		
CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA AGG AAC AAG ATC AGC	276	
Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser		
1 5 10		
AAA GAA TGC CAG CAG GTG TCC GGA GTG TCC CAA GAG ACG ATC GAC	321	
Lys Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp		
15 20 25		
AAA GTC CGC ACA GGT GTC TTG GTC GAT GAT CCC AAA ATG AAG AAG	366	
Lys Val Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys		
30 35 40		
CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA GTG GCA ACC GAA GCC	411	
His Val Leu Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala		
45 50 55		
GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC ACG CTG AAG CAT GTG	456	
Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu Lys His Val		
60 65 70		
GCC AGC GAC GAA GAA GTG GAC AAG ATC GTG CAG AAG TGC GTG GTC	501	
Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys Val Val		
75 80 85		
AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT CAC ACC TTC AAG TGT	546	
Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys Cys		
90 95 100		
Stop Codon		
ATT TAC GAC AGT AAA CCA GAT TTC TCT CCT ATT GAT TAA TTGTTTGTGA	595	
Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp *		
105 110 115		
Polyadenylation signal Poly-A tail		
TTTGACTGAA TTTTGACAT AAAGGTACTA TCGTTATGAA AAAAAAAAAA	645	
AAAAAAAACTC GAGGACACC ACCACCACTA CTGAGAT	682	

Fig. 5.9

His-tagged Clone 2.3 without signal sequence

TGTTAGCGG ATGGAATCC CTCGTAGGGG ATAATTTGT TTACTTTAAG	50
His-tag Start Codon	
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC	96
Met Gly Ser Ser His His His His His His Ser	
-30 -25	
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT	141
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly	
-20 -15 -10	
N-terminal of mature AFP	
GGA CAG CAA ATG GGT CGC GGA TCC CTC ACC GAC GAA CAG ATA CAG	186
Gly Gln Gln Met Gly Arg Gly Ser Leu Thr Asp Glu Gln Ile Gln	
-5 1 5	
AAA AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GTG TCC GGA GTG	231
Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val	
10 15 20	
TCC CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAT	276
Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp	
25 30 35	
GAT CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT	321
Asp Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr	
40 45 50	
GGA GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA	366
Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys	
55 60 65	
GCC AAG CTG AAG CAT GTG GCC AGC GAC GAA GAA GTG GAC AAG ATC	411
Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile	
70 75 80	
GTG CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT	456
Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala	
85 90 95	
TAT GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT	501
Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser	
100 105 110	
Stop Codon	
CCT ATT GAT TAA CTCGAGCACC ACCACCACCA CCACTGAGAT	543
Pro Ile Asp *	
115	

Fig. 5.10

His-tagged Tm 13 17 with signal sequence	
TTGTTAGCGG ATGGAATCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG	50
His-tag Start Codon	
AAGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC	96
Met Gly Ser Ser His His His His His Ser	
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AGC GGC CTG GTG CGG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT	141
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly	
-50 -45 -40	
GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC TGG ATC CAA AGA ATT	186
Gly Gln Gln Met Gly Arg Gly Ser Glu Phe Trp Ile Gln Arg Ile	
-35 -30 -25	
AFP Start Codon	
CGG CAC GAG ACT ACT AAG ATG AAG TTG CTC TGT TGT CTA ATC TCC	231
Arg His Glu Thr Thr Lys Met Lys Leu Leu Cys Cys Leu Ile Ser	
-20 -15 -10	
N-terminal of mature AFP	
CTC ATT CTG TTG GTC ACA GTT CAG GCC CTG ACC GAG GCA CAA ATT	276
Leu Ile Leu Leu Val Thr Val Gln Ala Leu Thr Glu Ala Gln Ile	
-5 1 5	
GAG AAA CTG AAC AAG ATC AGC AAA AAA TGT CAA AAT GAA AGT GGA	321
Glu Lys Leu Asn Lys Ile Ser Lys Lys Cys Gln Asn Glu Ser Gly	
10 15 20	
GTG TCG CAA GAG ATC ATA ACC AAA GCT CGC AAC GGT GAC TGG GAG	366
Val Ser Gln Glu Ile Ile Thr Lys Ala Arg Asn Gly Asp Trp Glu	
25 30 35	
GAC GAT CCT AAA CTG AAA CGC CAA GTT TTT TGC GTG GCC AGG AAC	411
Asp Asp Pro Lys Leu Lys Arg Gln Val Phe Cys Val Ala Arg Asn	
40 45 50	
GCC GGT CTG GCC ACG GAA TCG GGA GAG GTG GTG GTC GAC GTG TTG	456
Ala Gly Leu Ala Thr Glu Ser Gly Glu Val Val Val Asp Val Leu	
55 60 65	
AGG GAG AAG GTG AGG AAG GTC ACT GAC AAC GAC GAA GAA ACT GAG	501
Arg Glu Lys Val Arg Lys Val Thr Asp Asn Asp Glu Glu Thr Glu	
70 75 80	
AAA ATC ATC AAT AAG TGC GCC GTC AAG AGA GAT ACT GTT GAA GAG	546
Lys Ile Ile Asn Lys Cys Ala Val Lys Arg Asp Thr Val Glu Glu	
85 90 95	
ACG GTG TTC AAT ACT TTC AAA TGT GTC ATG AAA AAC CCA AAG	595
Thr Val Phe Asn Thr Phe Lys Cys Val Met Lys Asn Lys Pro Lys	
100 105 110	
Stop Codon	
TTC TCA CCA GTT GAT TGA ACCACCACGA CTAGTAGATG GTTCAATGG	643
Phe Ser Pro Val Asp *	
115	
Polyadenylation signal Poly-A tail	
TGTGCTTTAC ATATAAAAT AAAAGTGTTTC TGATGTAAAA AAAAAAAAAA	693
AAAAAAAAAA AACTCGAGAG TATTCTAGAG CGGCGCGGG CCATCGTTT	743
TCCACCCCTC GAGCACCACC ACCACCACCA CTGAGAT	777

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His-tag Start Codon	
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC	96
Met Gly Ser Ser His His His His His His Ser	
-30 -25	
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT	141
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly	
-20 -15 -10	
N-terminal of mature AFP	
GGA CAG CAA ATG GGT CGC GGC CTG ACC GAG GCA CAA ATT GAG AAA	186
Gly Gln Met Gly Arg Gly Leu Thr Glu Ala Gln Ile Glu Lys	
-5 1 5	
CTG AAC AAG ATC AGC AAA AAA TGT CAA AAT GAA AGT GGA GTG TCG	231
Leu Asn Lys Ile Ser Lys Lys Cys Gln Asn Glu Ser Gly Val Ser	
10 15 20	
CAA GAG ATC ATA ACC AAA GCT CGC AAC GGT GAC TGG GAG GAC GAT	276
Gln Glu Ile Ile Thr Lys Ala Arg Asn Gly Asp Trp Glu Asp Asp	
25 30 35	
CCT AAA CTG AAA CGC CAA GTT TTT TGC GTG GCC AGG AAC GCC GGT	321
Pro Lys Leu Lys Arg Gln Val Phe Cys Val Ala Arg Asn Ala Gly	
40 45 50	
CTG GCC ACG GAA TCG GGA GAG GTG GTG GTC GAC GTG TTG AGG GAG	366
Leu Ala Thr Glu Ser Gly Glu Val Val Val Asp Val Leu Arg Glu	
55 60 65	
AAG GTG AGG AAG GTC ACT GAC AAC GAC GAA GAA ACT GAG AAA ATC	411
Lys Val Arg Lys Val Thr Asp Asn Asp Glu Glu Thr Glu Lys Ile	
70 75 80	
ATC AAT AAG TGC GCC GTC AAG AGA GAT ACT GTT GAA GAG ACG GTG	456
Ile Asn Lys Cys Ala Val Lys Arg Asp Thr Val Glu Glu Thr Val	
85 90 95	
TTC AAT ACT TTC AAA TGT GTC ATG AAA AAC AAG CCA AAG TTC TCA	501
Phe Asn Thr Phe Lys Cys Val Met Lys Asn Lys Pro Lys Phe Ser	
100 105 110	
Stop Codon	
CCA GTT GAT TGA CTCGAGCACC ACCACCACCA CCACTGAGAT	543
Pro Val Asp *	
115	

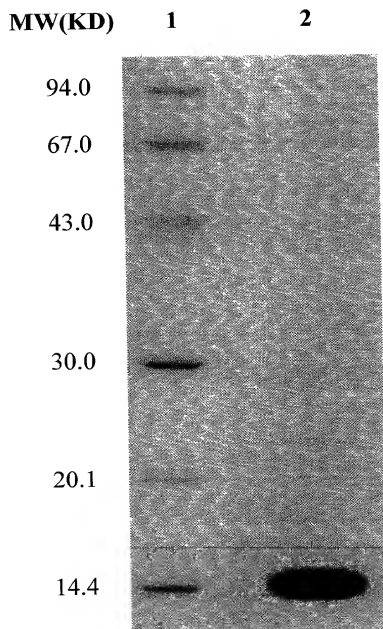


Fig. 6.0

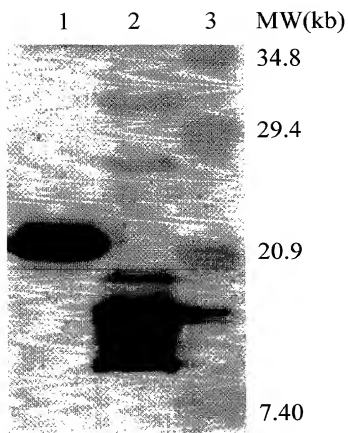
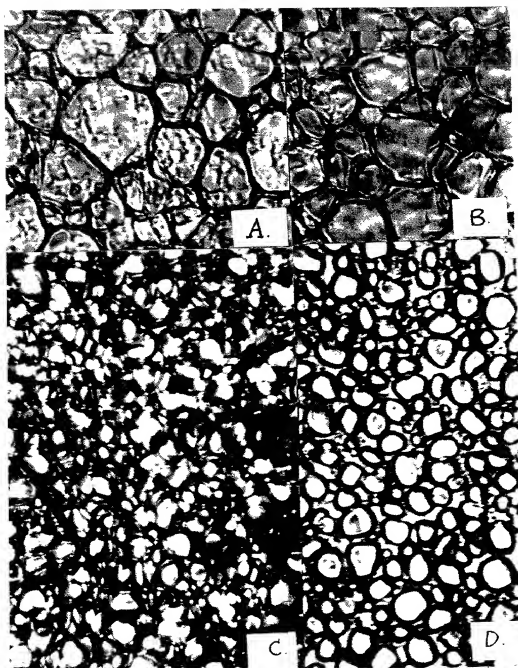


Fig. 6.1

*Fig. 6.2*

Tm 13.17 S-graph data

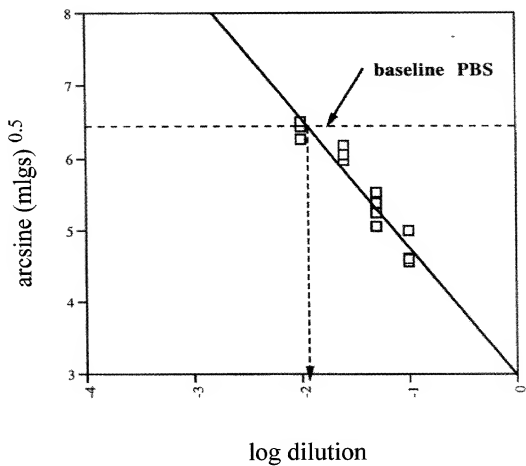


Fig. 6.3

ONE LETTER	NAME	THREE LETTER	CHEMICAL CLASS	HYDROPHOBICITY	Reactivity
A	Alanine	Ala	aliphatic	mod. hydrophobic	low
B	Asp or Asn	Asx			
C	Cysteine	Cys	sulfhydryl	hydrophobic	high
D	Aspartic Acid	Asp	acidic	highly hydrophilic	high
E	Glutamic Acid	Glu	acidic	highly hydrophilic	high
F	Phenylalanine	Phe	aromatic	highly hydrophobic	low
G	Glycine	Gly	aliphatic	mod. hydrophobic	low
H	Histidine	His	basic, imidazole	highly hydrophilic	high
I	Isoleucine	Ile	aliphatic	hydrophobic	low
J					
K	Lysine	Lys	basic	highly hydrophilic	high
L	Leucine	Leu	aliphatic	hydrophobic	low
M	Methionine	Met	sulfhydryl	hydrophobic	low
N	Asparagine	Asn	amide, acidic derived	hydrophilic	high
O					
P	Proline	Pro	aliphatic, cyclic, imino	mod. hydrophilic	low
Q	Glutamine	Gln	amide, acidic derived	hydrophilic	high
R	Arginine	Arg	basic	highly hydrophilic	high
S	Serine	Ser	aliphatic hydroxyl	hydrophilic	high
T	Threonine	Thr	aliphatic hydroxyl	hydrophilic	high
U					
V	Valine	Val	aliphatic	hydrophobic	low
W	Tryptophan	Trp	aromatic	highly hydrophobic	low
X					
Y	Tyrosine	Tyr	aromatic	mod. hydrophilic	high
Z	Glu or Gln	Glx			
		ACD	Any Acidic		
		ALP	Any Aliphatic		
		ALH	Any Aliphatic Hydroxyl		
		ARO	Any Aromatic		
		BAS	Any Basic		
		HY-	Hydrophobic		
		HY+	Hydrophilic		

Fig. 7.1

09070705 001200

Position	Tm12 84-2	Tm12 84-3	Tm12 84-4	Tm12 84-5	Tm12 84-6	Consensus of Tm12 84	Tm13 17	Consensus with Tm13 17	B1	Consensus with B1	APP-3	Consensus with APP-3
1	A	A	A	A	A	A	A	A			G	A
2	C	C	C	C	C	C	A	A			G	A
3	G	G	G	G	G	G	A	A			G	A
4	A	A	A	A	A	A	A	A			A	A
5	C	C	C	C	C	C	A	A			A	A
6	A	A	A	A	A	A	A	A			A	A
7	A	A	A	A	A	A	A	A			A	A
8	A	A	A	A	A	A	A	A			A	A
9	A	A	A	A	A	A	A	A			A	A
10	A	A	A	A	A	A	A	A			A	A
11	A	A	A	A	A	A	A	A			A	A
12	A	A	A	A	A	A	A	A			A	A
13	A	A	A	A	A	A	A	A			A	A
14	T	T	T	T	T	T	T	T			A	A
15	G	G	G	G	G	G	G	G			A	A
16	A	A	A	A	A	A	A	A			A	A
17	A	A	A	A	A	A	A	A			A	A
18	A	A	A	A	A	A	A	A			A	A
19	C	C	C	C	C	C	C	C			A	A
20	C	C	C	C	C	C	C	C			A	A
21	C	C	C	C	C	C	C	C			A	A
22	C	C	C	C	C	C	C	C			A	A
23	C	C	C	C	C	C	C	C			A	A
24	C	C	C	C	C	C	C	C			A	A
25	T	T	T	T	T	T	T	T			A	A
26	T	T	T	T	T	T	T	T			A	A
27	T	T	T	T	T	T	T	T			A	A
28	T	T	T	T	T	T	T	T			A	A
29	T	T	T	T	T	T	T	T			A	A
30	T	T	T	T	T	T	T	T			A	A
31	T	T	T	T	T	T	T	T			A	A
32	T	T	T	T	T	T	T	T			A	A
33	T	T	T	T	T	T	T	T			A	A
34	T	T	T	T	T	T	T	T			A	A
35	T	T	T	T	T	T	T	T			A	A
36	T	T	T	T	T	T	T	T			A	A
37	T	T	T	T	T	T	T	T			A	A
38	T	T	T	T	T	T	T	T			A	A
39	T	T	T	T	T	T	T	T			A	A
40	T	T	T	T	T	T	T	T			A	A
41	T	T	T	T	T	T	T	T			A	A
42	T	T	T	T	T	T	T	T			A	A
43	T	T	T	T	T	T	T	T			A	A
44	T	T	T	T	T	T	T	T			A	A
45	T	T	T	T	T	T	T	T			A	A
46	T	T	T	T	T	T	T	T			A	A
47	T	T	T	T	T	T	T	T			A	A
48	T	T	T	T	T	T	T	T			A	A
49	T	T	T	T	T	T	T	T			A	A
50	T	T	T	T	T	T	T	T			A	A
51	T	T	T	T	T	T	T	T			A	A
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53	T	T	T	T	T	T	T	T			A	A
54	T	T	T	T	T	T	T	T			A	A
55	T	T	T	T	T	T	T	T			A	A
56	T	T	T	T	T	T	T	T			A	A
57	T	T	T	T	T	T	T	T			A	A
58	T	T	T	T	T	T	T	T			A	A
59	T	T	T	T	T	T	T	T			A	A
60	T	T	T	T	T	T	T	T			A	A
61	T	T	T	T	T	T	T	T			A	A
62	T	T	T	T	T	T	T	T			A	A
63	T	T	T	T	T	T	T	T			A	A
64	T	T	T	T	T	T	T	T			A	A
65	T	T	T	T	T	T	T	T			A	A
66	T	T	T	T	T	T	T	T			A	A
67	T	T	T	T	T	T	T	T			A	A
68	T	T	T	T	T	T	T	T			A	A
69	T	T	T	T	T	T	T	T			A	A
70	T	T	T	T	T	T	T	T			A	A
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72	T	T	T	T	T	T	T	T			A	A
73	T	T	T	T	T	T	T	T			A	A
74	T	T	T	T	T	T	T	T			A	A
75	T	T	T	T	T	T	T	T			A	A
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77	T	T	T	T	T	T	T	T			A	A
78	T	T	T	T	T	T	T	T			A	A
79	T	T	T	T	T	T	T	T			A	A
80	T	T	T	T	T	T	T	T			A	A
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82	T	T	T	T	T	T	T	T			A	A
83	T	T	T	T	T	T	T	T			A	A
84	T	T	T	T	T	T	T	T			A	A
85	T	T	T	T	T	T	T	T			A	A
86	T	T	T	T	T	T	T	T			A	A
87	T	T	T	T	T	T	T	T			A	A
88	T	T	T	T	T	T	T	T			A	A
89	T	T	T	T	T	T	T	T			A	A
90	T	T	T	T	T	T	T	T			A	A
91	T	T	T	T	T	T	T	T			A	A
92	T	T	T	T	T	T	T	T			A	A
93	T	T	T	T	T	T	T	T			A	A
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95	T	T	T	T	T	T	T	T			A	A
96	T	T	T	T	T	T	T	T			A	A
97	T	T	T	T	T	T	T	T			A	A
98	T	T	T	T	T	T	T	T			A	A
99	T	T	T	T	T	T	T	T			A	A
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109	T	T	T	T	T	T	T	T			A	A
110	T	T	T	T	T	T	T	T			A	A
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113	T	T	T	T	T	T	T	T			A	A
114	T	T	T	T	T	T	T	T			A	A
115	T	T	T	T	T	T	T	T			A	A
116	T	T	T	T	T	T	T	T			A	A
117	T	T	T	T	T	T	T	T			A	A

Fig. 7.2

Position	Tm12 64-23	Tm12 84-23	Tm12 84-34	Tm12 84-39	Tm12 84-76	Consensus of	Tm12 17	Consensus with	B1	Consensus with	AFP-3	Consensus with
118	C	C	C	C	C	C	N	N	C	N	C	N
119	A	A	A	A	A	A	A	A	C	N	C	N
120	G	G	G	G	G	G	G	G	G	G	G	G
121	G	G	G	G	G	G	G	G	G	G	G	G
122	T	T	T	T	T	T	T	T	T	T	T	T
123	G	G	G	G	G	G	G	G	G	G	G	G
124	T	T	T	T	T	T	T	T	T	T	T	T
125	C	C	C	C	C	C	C	C	C	C	C	C
126	G	G	G	G	G	G	G	G	G	G	G	G
127	G	G	G	G	G	G	G	G	G	G	G	G
128	A	A	A	A	A	A	A	A	A	A	A	A
129	T	T	T	T	T	T	T	T	T	T	T	T
130	T	T	T	T	T	T	T	T	T	T	T	T
131	T	T	T	T	T	T	T	T	T	T	T	T
132	T	T	T	T	T	T	T	T	T	T	T	T
133	C	C	C	C	C	C	C	C	C	C	C	C
134	C	C	C	C	C	C	C	C	C	C	C	C
135	C	C	C	C	C	C	C	C	C	C	C	C
136	A	A	A	A	A	A	A	A	A	A	A	A
137	A	A	A	A	A	A	A	A	A	A	A	A
138	A	A	A	A	A	A	A	A	A	A	A	A
139	A	A	A	A	A	A	A	A	A	A	A	A
140	A	A	A	A	A	A	A	A	A	A	A	A
141	A	A	A	A	A	A	A	A	A	A	A	A
142	A	A	A	A	A	A	A	A	A	A	A	A
143	A	A	A	A	A	A	A	A	A	A	A	A
144	A	A	A	A	A	A	A	A	A	A	A	A
145	A	A	A	A	A	A	A	A	A	A	A	A
146	T	T	T	T	T	T	T	T	T	T	T	T
147	G	G	G	G	G	G	G	G	G	G	G	G
148	A	A	A	A	A	A	A	A	A	A	A	A
149	A	A	A	A	A	A	A	A	A	A	A	A
150	A	A	A	A	A	A	A	A	A	A	A	A
151	A	A	A	A	A	A	A	A	A	A	A	A
152	A	A	A	A	A	A	A	A	A	A	A	A
153	A	A	A	A	A	A	A	A	A	A	A	A
154	A	A	A	A	A	A	A	A	A	A	A	A
155	T	T	T	T	T	T	T	T	T	T	T	T
156	T	T	T	T	T	T	T	T	T	T	T	T
157	G	G	G	G	G	G	G	G	G	G	G	G
158	C	C	C	C	C	C	C	C	C	C	C	C
159	C	C	C	C	C	C	C	C	C	C	C	C
160	C	C	C	C	C	C	C	C	C	C	C	C
161	C	C	C	C	C	C	C	C	C	C	C	C
162	C	C	C	C	C	C	C	C	C	C	C	C
163	G	G	G	G	G	G	G	G	G	G	G	G
164	G	G	G	G	G	G	G	G	G	G	G	G
165	T	T	T	T	T	T	T	T	T	T	T	T
166	T	T	T	T	T	T	T	T	T	T	T	T
167	T	T	T	T	T	T	T	T	T	T	T	T
168	T	T	T	T	T	T	T	T	T	T	T	T
169	T	T	T	T	T	T	T	T	T	T	T	T
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172	T	T	T	T	T	T	T	T	T	T	T	T
173	T	T	T	T	T	T	T	T	T	T	T	T
174	T	T	T	T	T	T	T	T	T	T	T	T
175	T	T	T	T	T	T	T	T	T	T	T	T
176	T	T	T	T	T	T	T	T	T	T	T	T
177	T	T	T	T	T	T	T	T	T	T	T	T
178	T	T	T	T	T	T	T	T	T	T	T	T
179	T	T	T	T	T	T	T	T	T	T	T	T
180	T	T	T	T	T	T	T	T	T	T	T	T
181	T	T	T	T	T	T	T	T	T	T	T	T
182	T	T	T	T	T	T	T	T	T	T	T	T
183	T	T	T	T	T	T	T	T	T	T	T	T
184	T	T	T	T	T	T	T	T	T	T	T	T
185	T	T	T	T	T	T	T	T	T	T	T	T
186	T	T	T	T	T	T	T	T	T	T	T	T
187	T	T	T	T	T	T	T	T	T	T	T	T
188	T	T	T	T	T	T	T	T	T	T	T	T
189	T	T	T	T	T	T	T	T	T	T	T	T
190	T	T	T	T	T	T	T	T	T	T	T	T
191	T	T	T	T	T	T	T	T	T	T	T	T
192	T	T	T	T	T	T	T	T	T	T	T	T
193	T	T	T	T	T	T	T	T	T	T	T	T
194	T	T	T	T	T	T	T	T	T	T	T	T
195	T	T	T	T	T	T	T	T	T	T	T	T
196	T	T	T	T	T	T	T	T	T	T	T	T
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216	T	T	T	T	T	T	T	T	T	T	T	T
217	T	T	T	T	T	T	T	T	T	T	T	T
218	T	T	T	T	T	T	T	T	T	T	T	T
219	T	T	T	T	T	T	T	T	T	T	T	T
220	T	T	T	T	T	T	T	T	T	T	T	T
221	T	T	T	T	T	T	T	T	T	T	T	T
222	T	T	T	T	T	T	T	T	T	T	T	T
223	T	T	T	T	T	T	T	T	T	T	T	T
224	T	T	T	T	T	T	T	T	T	T	T	T
225	T	T	T	T	T	T	T	T	T	T	T	T
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227	T	T	T	T	T	T	T	T	T	T	T	T
228	T	T	T	T	T	T	T	T	T	T	T	T
229	T	T	T	T	T	T	T	T	T	T	T	T
230	T	T	T	T	T	T	T	T	T	T	T	T
231	T	T	T	T	T	T	T	T	T	T	T	T
232	T	T	T	T	T	T	T	T	T	T	T	T
233	T	T	T	T	T	T	T	T	T	T	T	T
234	T	T	T	T	T	T	T	T	T	T	T	T
235	T	T	T	T	T	T	T	T	T	T	T	T

Fig. 7.2 cont.

[illegible]

Fig. 7.2 cont.

[illegible]

Fig. 7.2 cont.

Position	Tm12 84-2-2	Tm12 84-2-3	Tm12 84-3-4	Tm12 84-3-9	Tm12 84-7-5	Consensus of	Tm12 17	Consensus with	B1	Consensus with	AFP-3	Consensus with
472	A	A	A	A	A	A	A	A		A	A	A
473	A	A	A	A	A	A	A	A		A	A	A
474	T	T	T	T	T	T	T	T		T	T	T
475	A	A	A	A	A	A	A	A		A	A	A
476	A	A	A	A	A	A	A	A		A	A	A
477	A	A	A	A	A	A	A	A		A	A	A
478	G	G	G	G	G	G	G	G		G	G	G
479	G	G	G	G	G	G	T	N		N	T	N
480	T	T	T	T	T	T	T	T		N	T	N
481	A	A	A	A	A	A	T	N		N	T	N
482	A	C	C	C	C	C	T	Y		Y	A	M
483	T	T	T	T	T	T	T	T		T	A	AT
484	A	T	A	A	T	A	T	C		N	C	M
485	T	T	T	T	T	T	T	T		T	A	AT
486	C	C	C	C	C	C	G	T		N	A	N
487	G	G	G	G	G	G	A	B		N	A	N
488	T	T	T	T	T	T	T	T		T	A	TA
489	A	A	A	A	A	A	A	A		N	A	N
490	T	T	T	T	T	T	A	N		N	A	N
491	T	T	T	T	T	T	A	N		N	A	N
492	T	G	G	G	G	G	A	R		R	A	N
493	T	A	A	A	T	N	A	N		N	A	A
494	A	A	A	A	A	A	A	A		A	A	A
495	A	A	A	A	A	A	A	A		A	A	A
496	A	A	A	A	A	A	A	A		A	A	A
497	A	A	A	A	A	A	A	A		A	A	A
498	A	A	A	A	A	A	A	A		A	A	A
499	A	A	A	A	A	A	A	A		A	A	A
500	A	A	A	A	A	A	A	A		A	A	A
501	A	A	A	A	A	A	A	A		A	A	A
502	A	A	A	A	A	A	A	A		A	A	A
503	A	A	A	A	A	A	A	A		A	A	A
504	A	A	A	A	A	A	A	A		A	A	A
505	A	A	A	A	A	A	A	A		A	A	A
506	A	A	A	A	A	A	A	A		A	A	A
507	A	A	A	A	A	A	A	A		A	A	A
508	A	A	A	A	A	A	A	A		A	A	A
509	A	A	A	A	A	A	A	A		A	A	A
510	A	A	A	A	A	A	A	A		A	A	A
511	A	A	A	A	A	A	A	A		A	A	A
512												

00076736.021202

Fig. 7.2 cont.

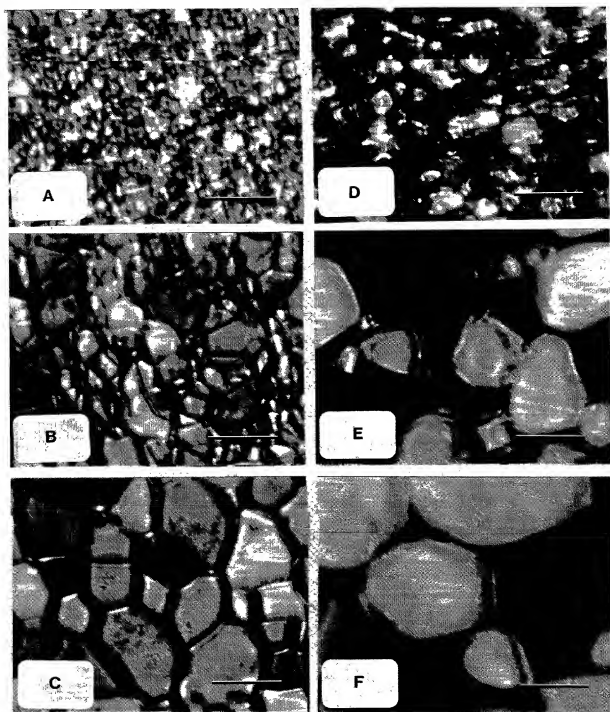


Fig. 8.0

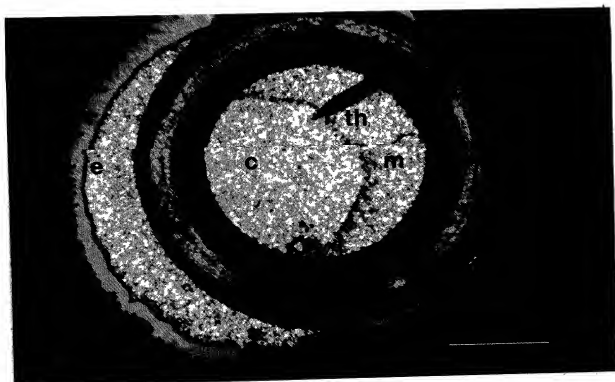


Fig. 8.1a

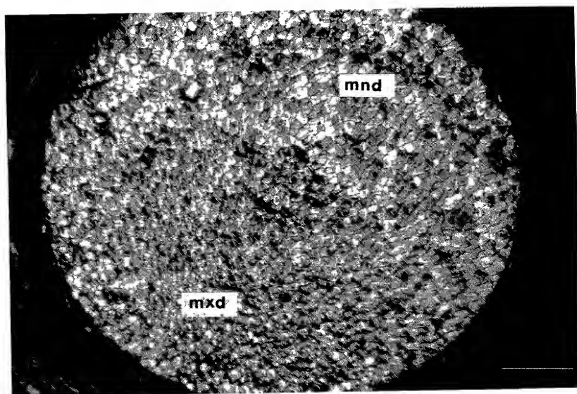


Fig. 8.1b

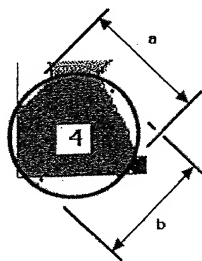
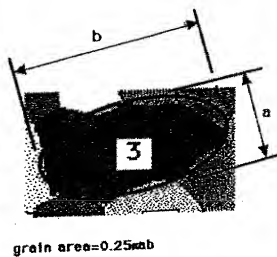
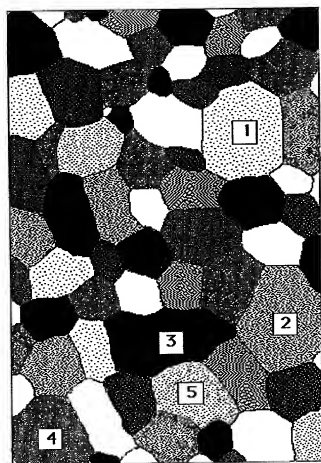
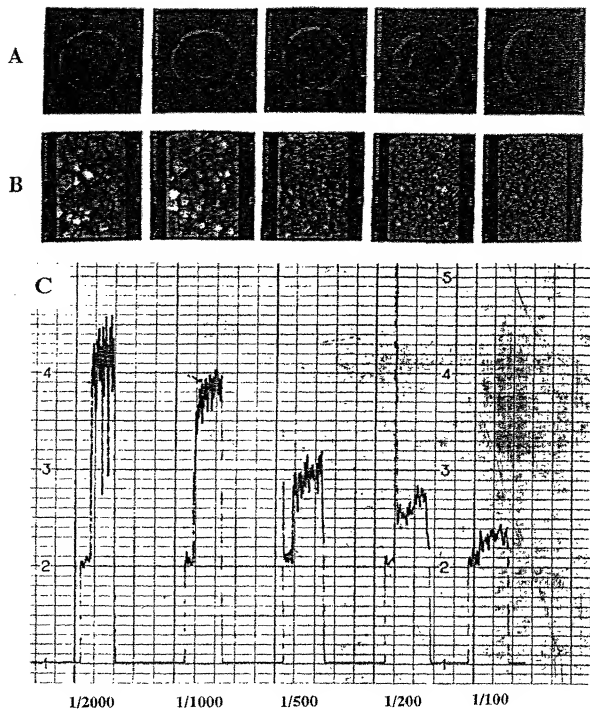


Fig. 8.2

*Fig. 8.3*

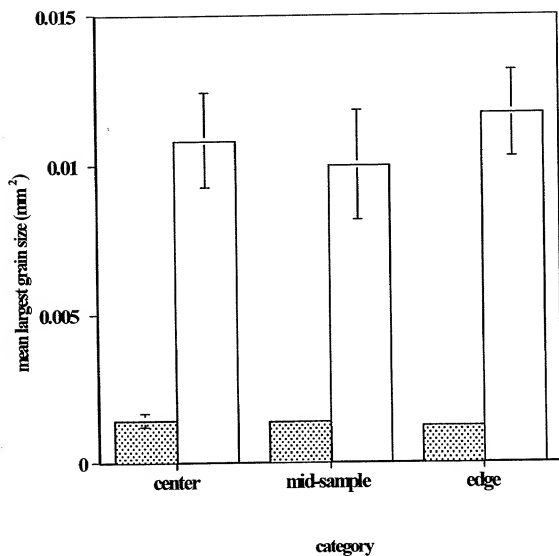


Fig. 8.4a

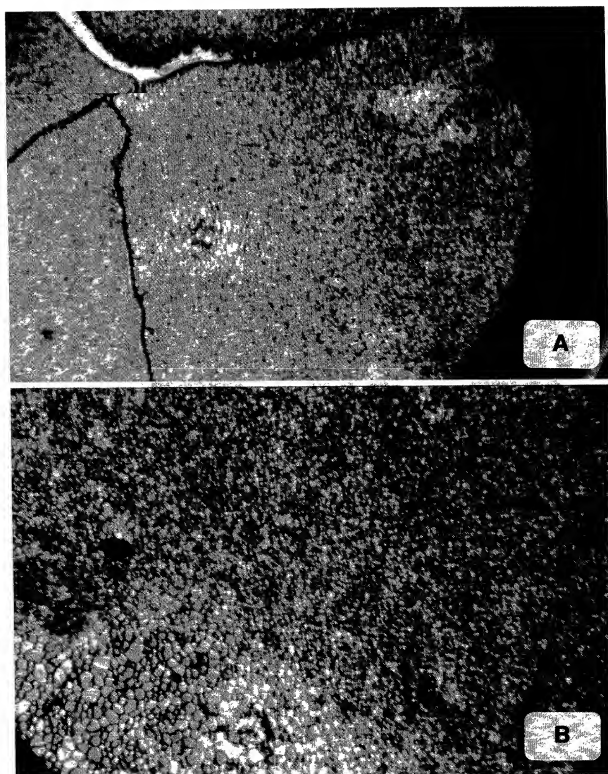
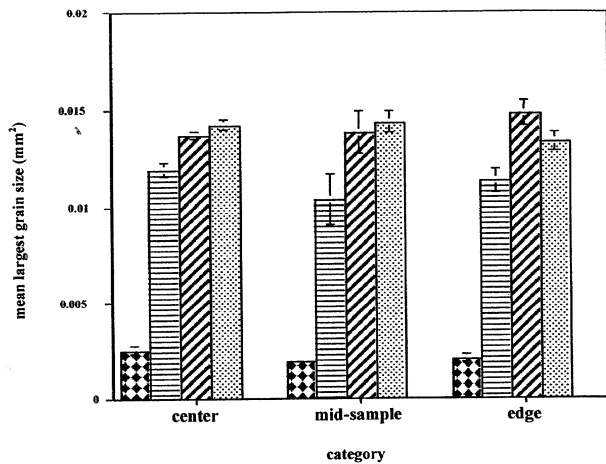


Fig. 8.46

*Fig. 8.5a*

09876796.0212021

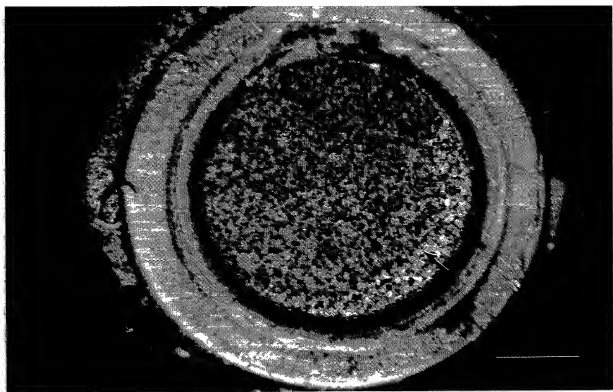
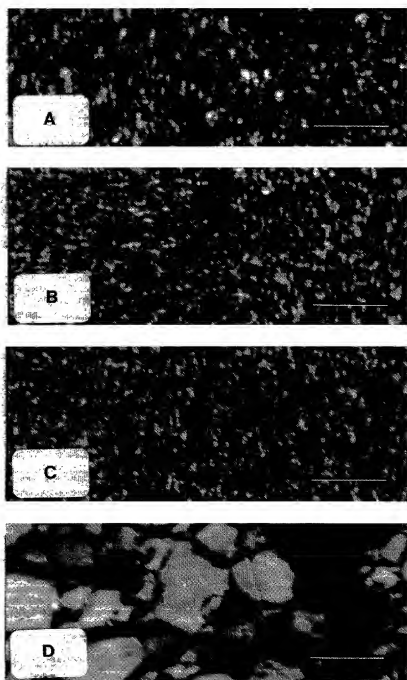


Fig. 8.5b

*Fig. 8.6*

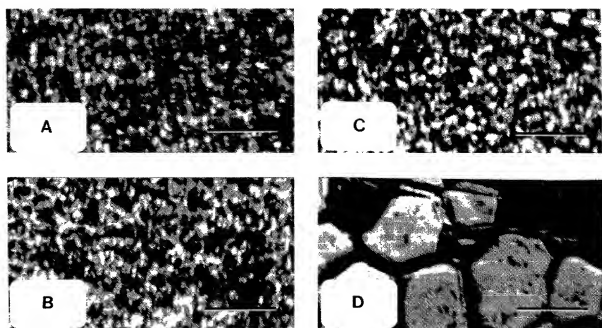


Fig. 8.7

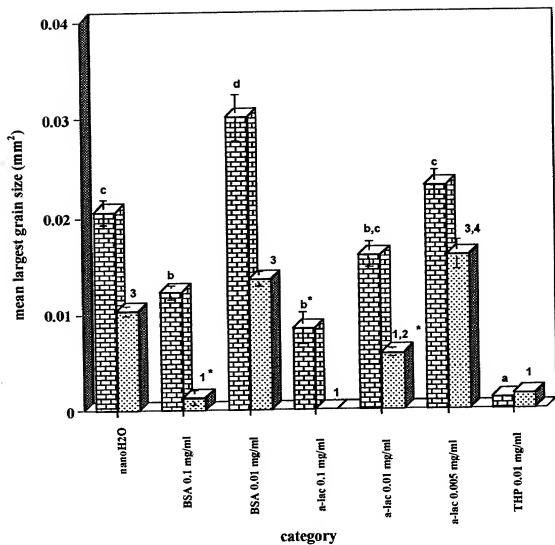
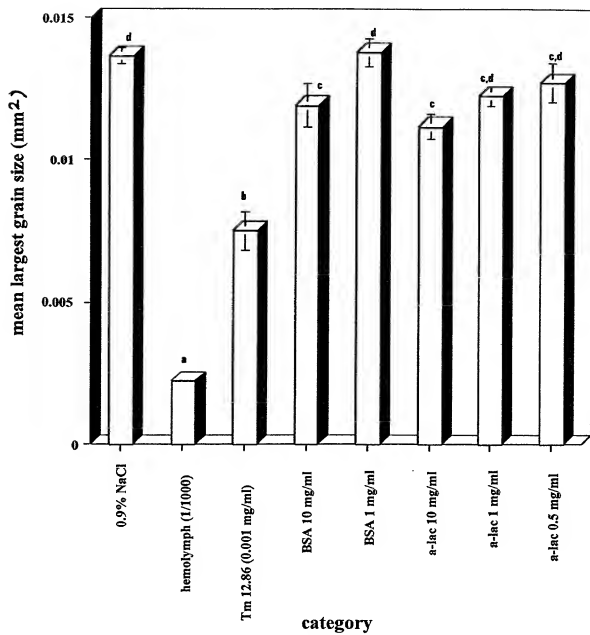


Fig. 8.8

*Fig. 8.9*

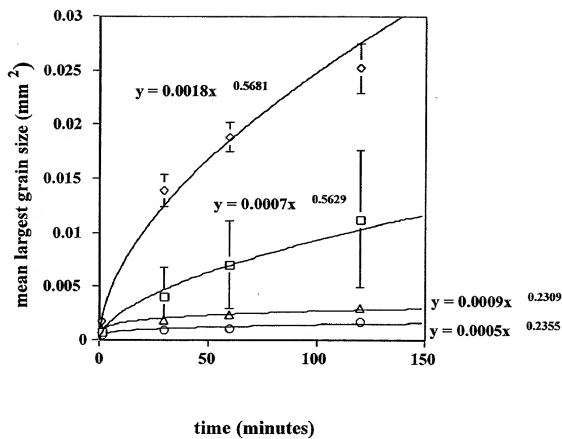
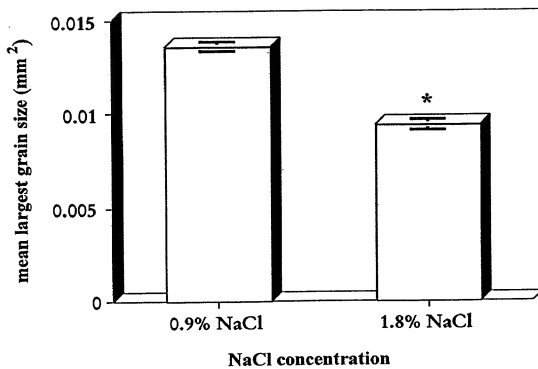


Fig. 8.10

*Fig. 8.11*

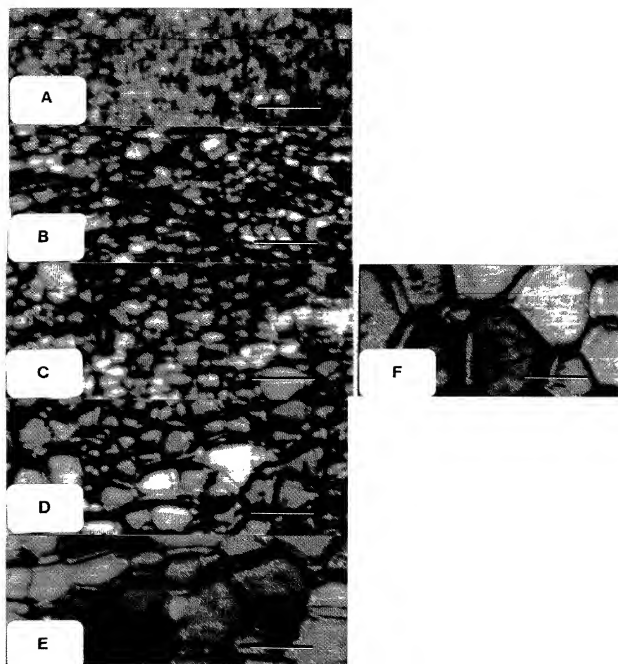
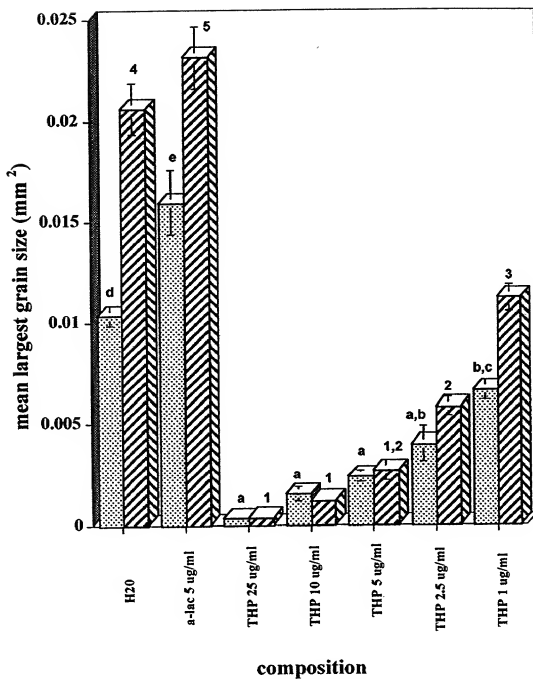
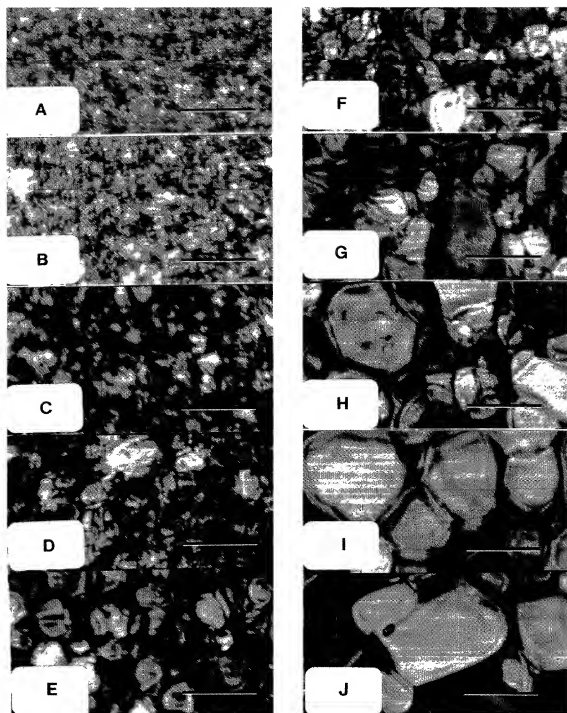


Fig. 8.12

*Fig. 8.13*

*Fig. 8.14*

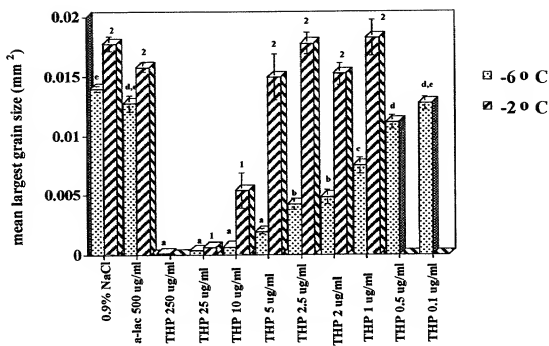


Fig. 8.15

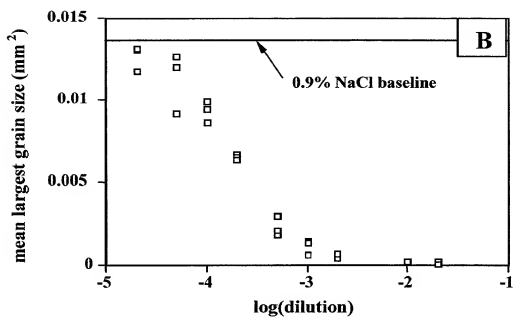
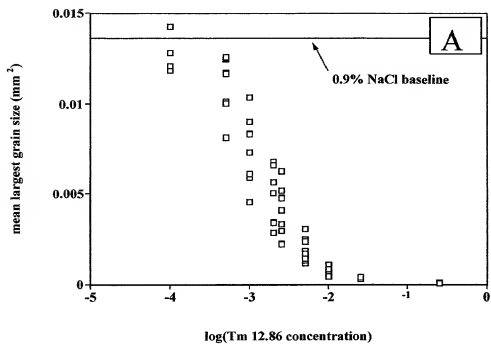
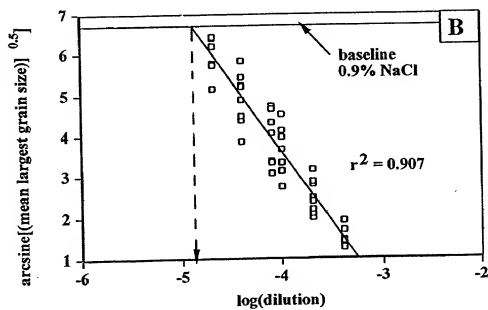
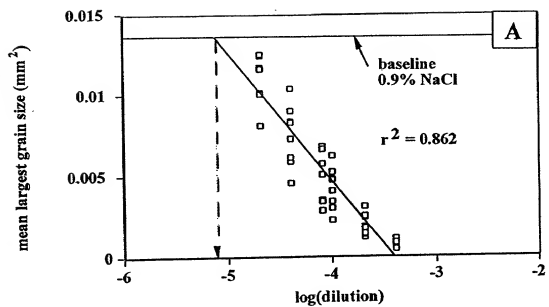
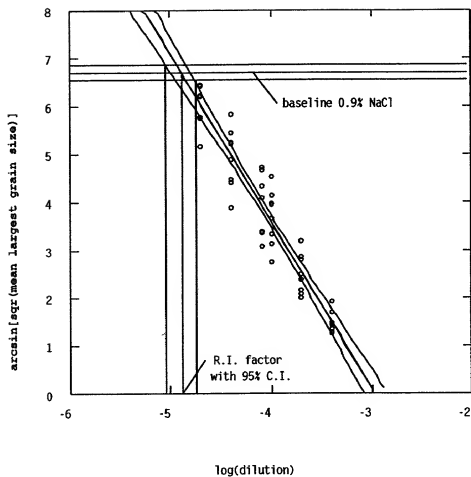


Fig. 8.16

*Fig. 8.17*

*Fig. 8.18*

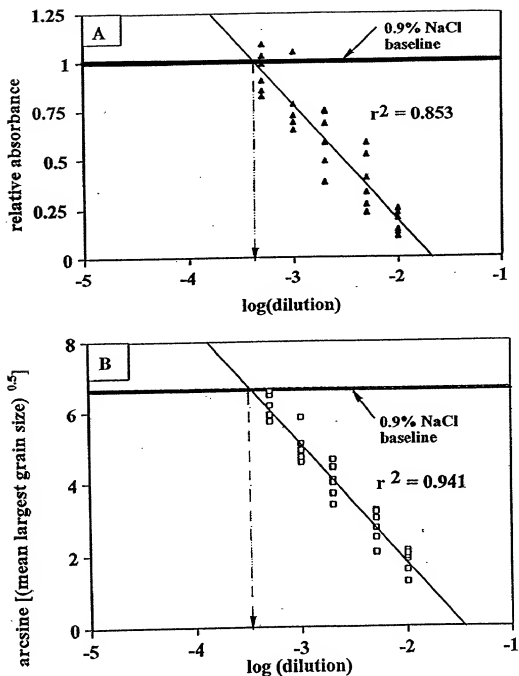
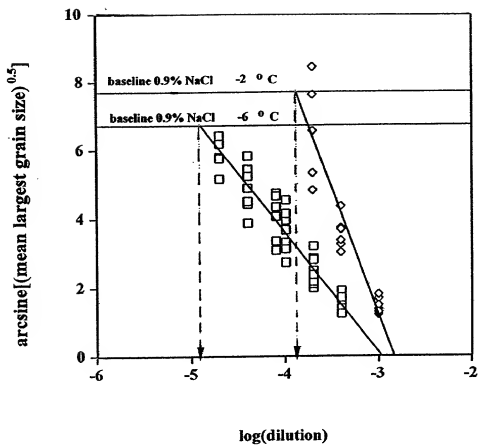


Fig. 8.19

*Fig. 8.20*

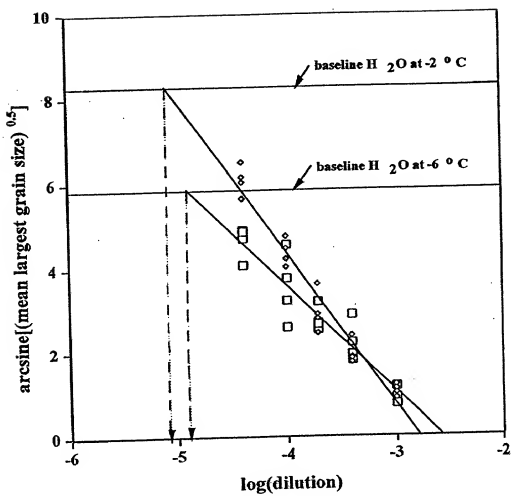
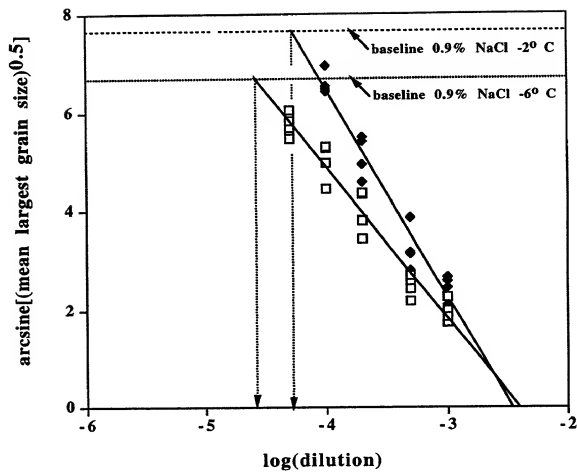
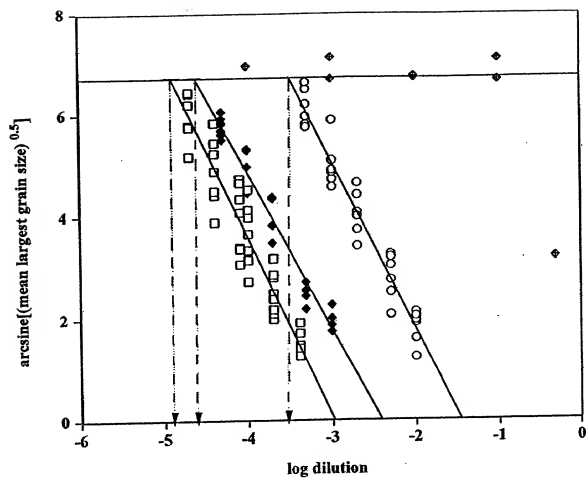


Fig. 8.21

*Fig. 8.22*

*Fig. 8.23*

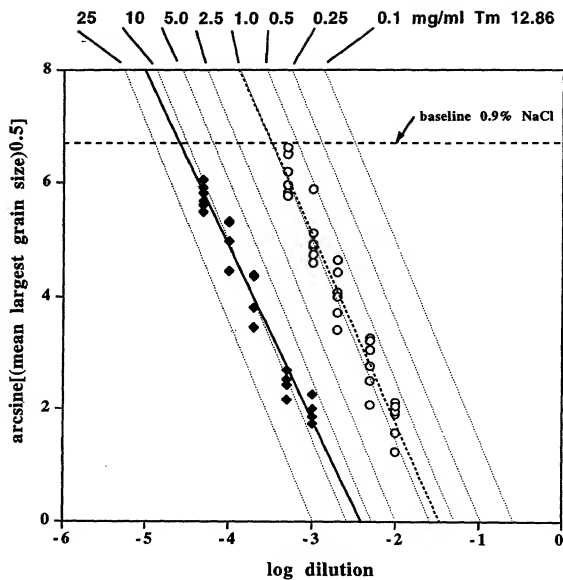
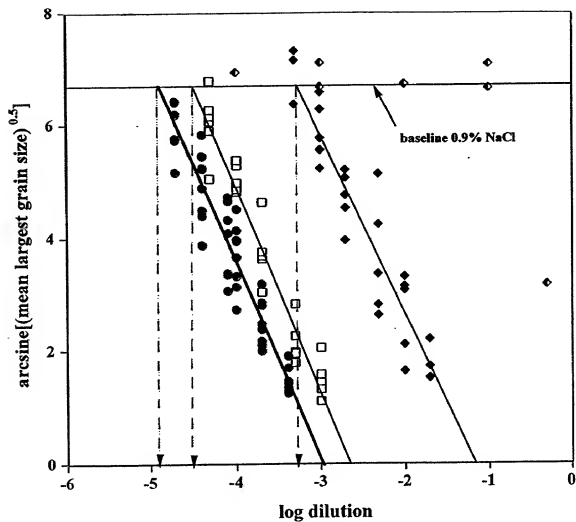
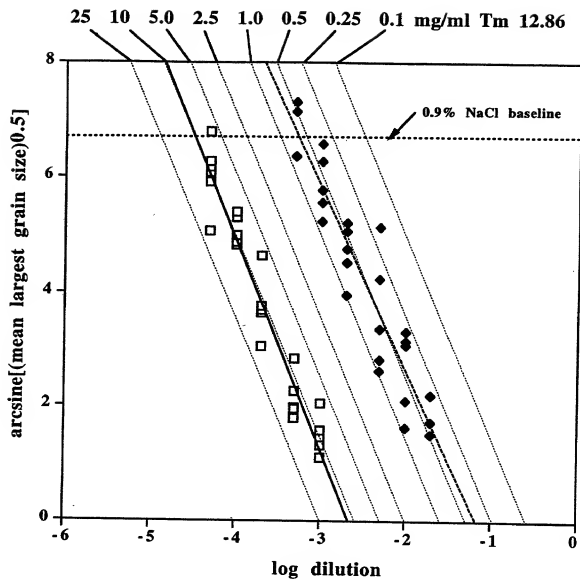
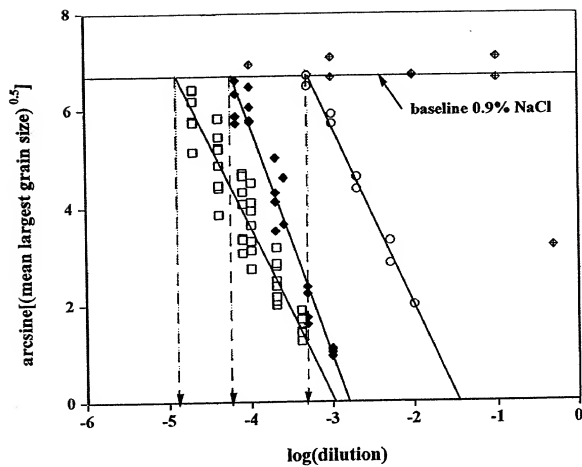
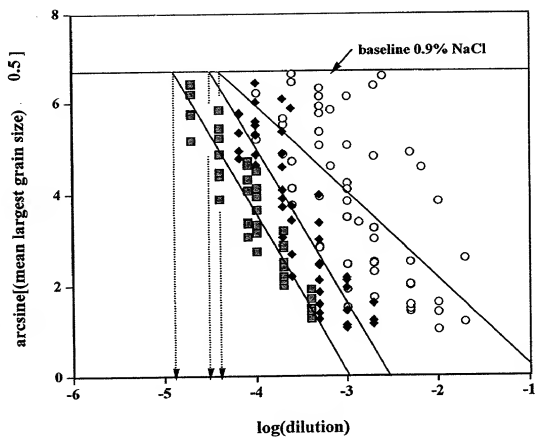


Fig. 8.24

*Fig. 8.25*

*Fig. 8.26*

*Fig. 8.27*

*Fig. 8.28*

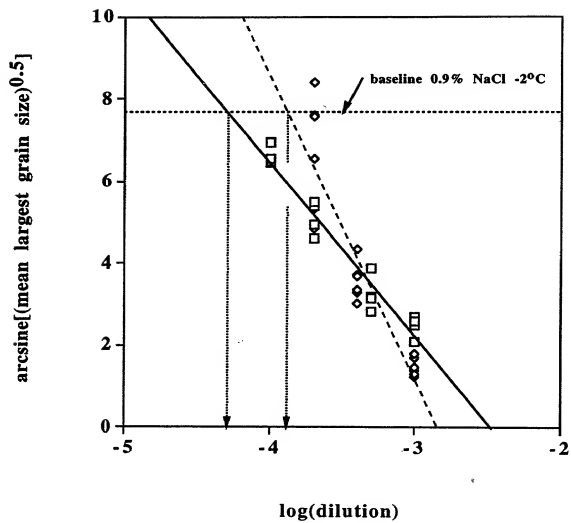
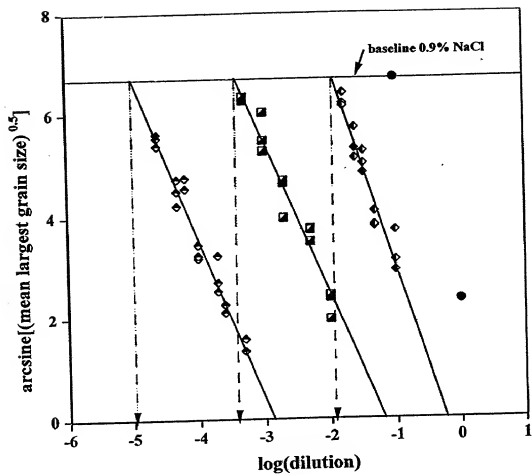


Fig. 8.29

*Fig. 8.30*

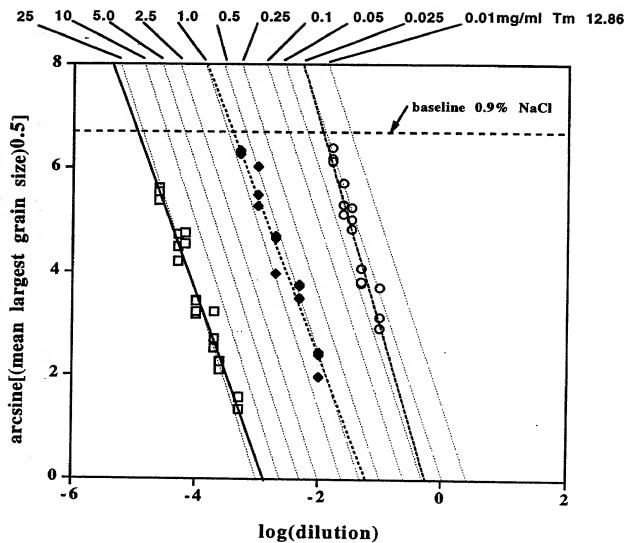


Fig. 8.31

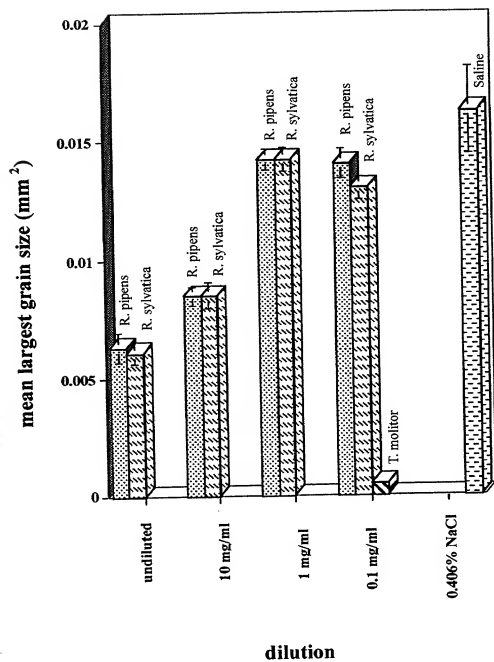
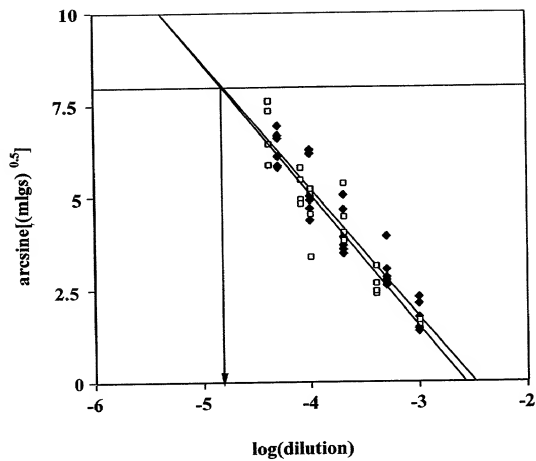
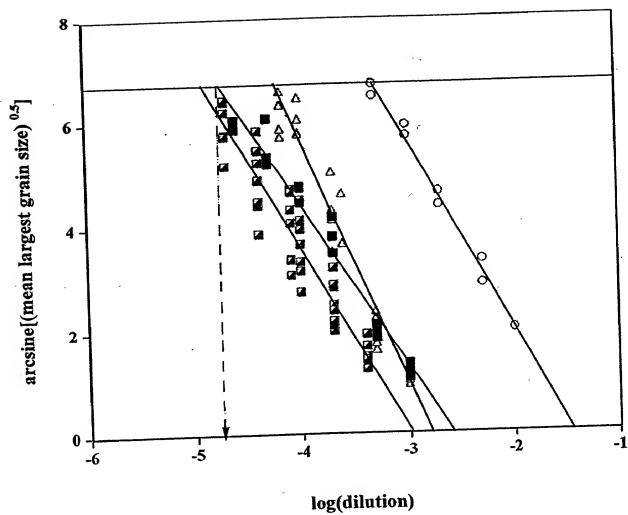
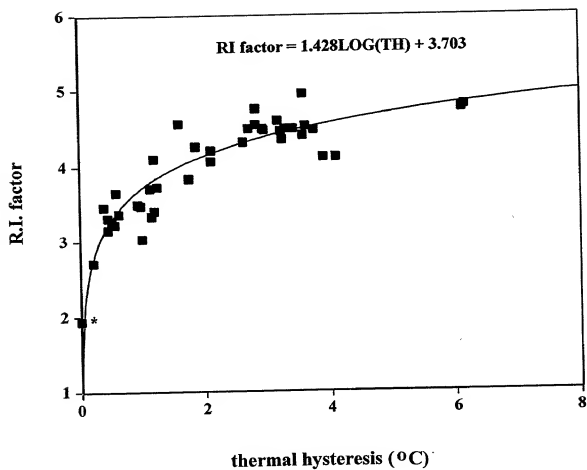


Fig. 8.32

*Fig. 8.33*

*Fig. 8.34*

*Fig. 8.35*

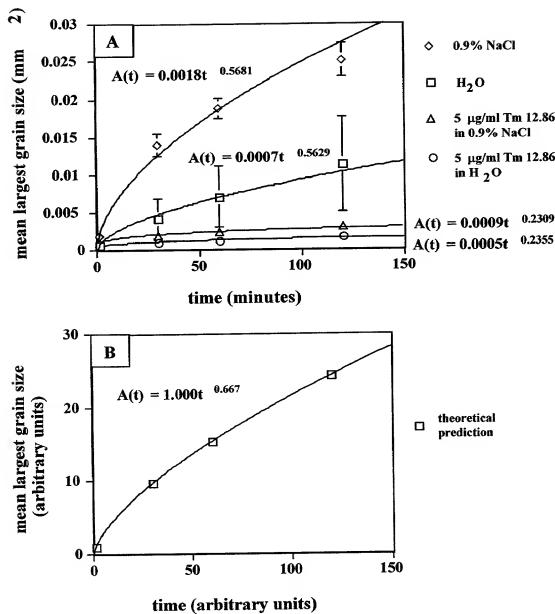


Fig. 8.36

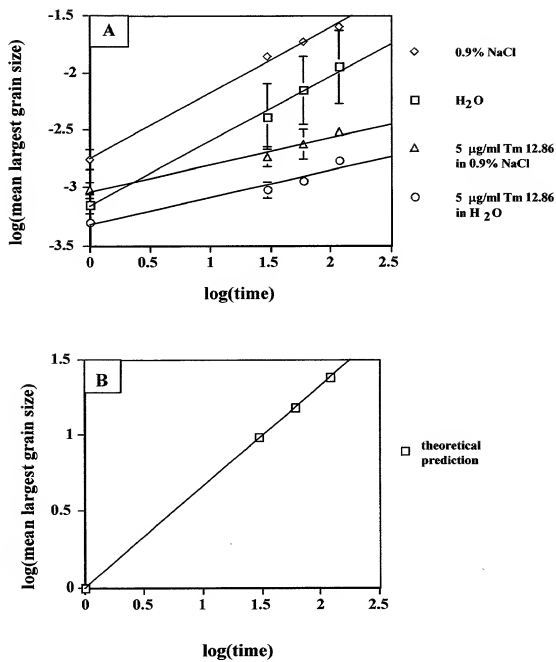
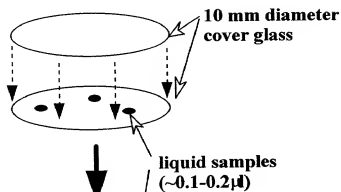


Fig. 8.37

"Sandwich" method of R.I. assessment

1.



2.



3. FREEZE ON $\sim -80^{\circ}\text{C}$
ALUMINUM PLATE (~ 10 MIN.)

4. PLACE ON COLD STAGE,
ANNEAL AT -6°C UP TO
12+ HOURS

Fig. 8.38

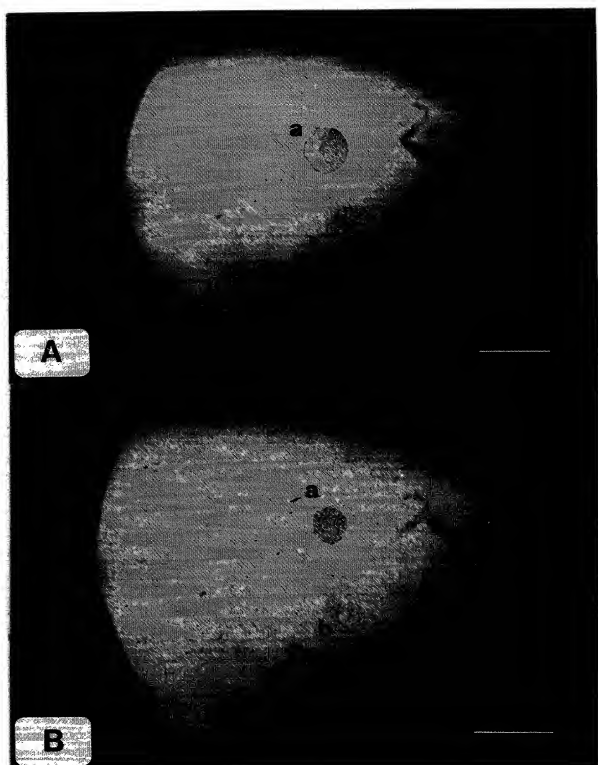


Fig. 8.39

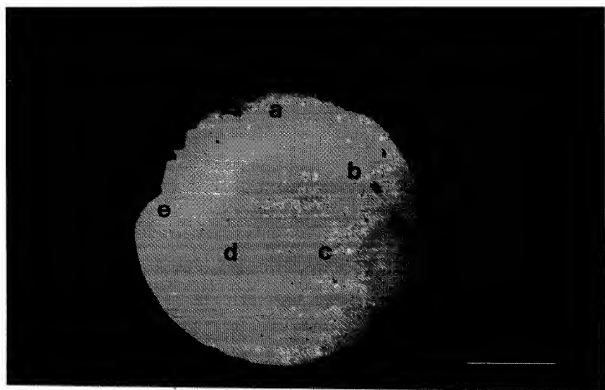
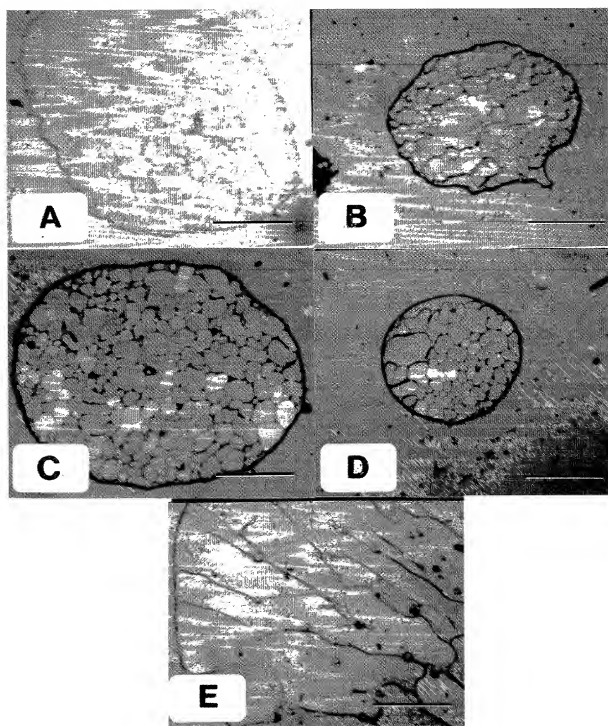
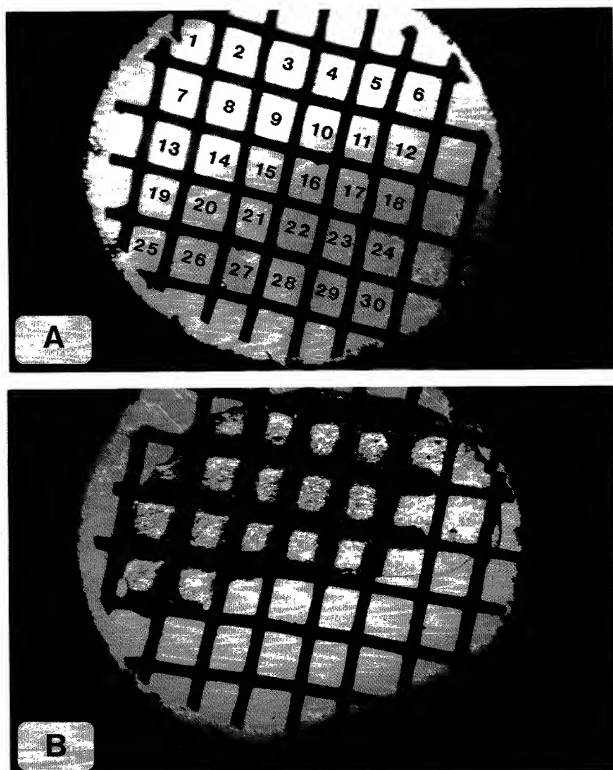


Fig. 8.40

*Fig. 8.41*

*Fig. 8.42*

[illegible]X
b
o
i

Fig. 8.43

1 GGCACGAGCAAAA ATGAAACTCCTCTTGTGCTTTG CGTTCGCCGCC
M K L L L C F A F A A

47 ATCGTCATGGGGAGCTCAGGCT CTCACCGACGAACAGATACAGAAA
I V I G A Q A L T D E Q I Q K

92 AGGAACAAGATCAGCAAAGAATGCCAGCAGGTGTCC GGAGTGTCC
R N K I S K E C Q Q V S G V S

137 CAAGAGACGATCGACAAAGTCCGCACAGGTGTCTTGGTCGATGAT
Q E T I D K V R T G V L V D D

182 CCCAAAATGAAGAAGCACGTCCTCTGCTTCTCGAAGAAAACCTGGA
P K M K K H V L C F S K K T G

226 GTGGCAACCGAAGCCGGAGACACCAATGTGGAGGTACTCAAAGCC
V A T E A G D T N V E V L K A

271 AAGCTGAAGCATGTGGCCAGCGACGAAGAGGTGGACAAGATCGTG
K L K H V A S D E E V D K I V

316 CAGAAGTGCGTGGTCAAGAAGGCC ACACCAGAGGAAACGGCTTAT
Q K C V V K K A T P E E T A Y

361 GACACCTTCAAGTGATTTACGACAGCAAACCTGATTT CTCTCCT
D T F K C I Y D S K P D F S P

406 ATTGATTAATTGTTTTGATTTGACTGAATTTTGACAATAAAGGT
I D

451 ACTATCGTTATGTAAAAAAAAAAAAAAAAAAAA

polyadenylation signal

poly (A) tail

Fig. 8.44